

Db 1 DIQMTSPSTLSASVGDRTVITCKASQDINRYLNMWQKPKAKPLIYRANRLVDGVPS 60
QY 61 RFSGSGSGDYTLTITSSLOPDPFATYVCLOFHEFPYFGGTTLEIK 107
Db 61 RFSGSGSGTEFTLTITSSLOPDPFATYVCLOFHEFPYFGGTTLEIK 107

RESULT 2
PCT-US95-10053-17
Sequence 17, Application PC/TUS9510053

GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytial
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10053
FILING DATE: Concurrently
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 469201-274
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US95-10053-17

Query Match 90.9%; Score 510; DB 5; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.2e-44;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTSPSTLSASVGDRTVITCKASQDINRYLNMWQKPKAKPLIYRANRLVDGVPS 60
Db 1 DIQMTSPSTLSASVGDRTVITCKASQDINRYLNMWQKPKAKPLIYRANRLVDGVPS 60
QY 61 RFSGSGSGDYTLTITSSLOPDPFATYVCLOFHEFPYFGGTTLEIK 107
Db 61 RFSGSGSGTEFTLTITSSLOPDPFATYVCLOFHEFPYFGGTTLEIK 107

RESULT 3
PCT-US96-09448-20
Sequence 20, Application PC/TUS9609448
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against Respiratory Syncytial
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09448
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 469201-257
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US96-09448-20

Query Match 90.9%; Score 510; DB 5; Length 107;
Best Local Similarity 88.8%; Pred. No. 4.2e-44;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIQMTSPSTLSASVGDRTVITCKASQDINRYLNMWQKPKAKPLIYRANRLVDGVPS 60
Db 1 DIQMTSPSTLSASVGDRTVITCKASQDINRYLNMWQKPKAKPLIYRANRLVDGVPS 60
QY 61 RFSGSGSGDYTLTITSSLOPDPFATYVCLOFHEFPYFGGTTLEIK 107
Db 61 RFSGSGSGTEFTLTITSSLOPDPFATYVCLOFHEFPYFGGTTLEIK 107

RESULT 4
US-08-107-669D-27
Sequence 27, Application US/08107669D
Patent No. 576886
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D

```

; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-107-669D-27

Query Match      89.5%; Score 502; DB 1; Length 107;
Best Local Similarity 88.8%; Pred. No. 2.6e-43;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Cy 1 DIQWTGSPSSLSASVGDRTVITCKASQDINSYLSWFOQKPKAKPTLIYRANRLVDGVPS 60
Db 1 DIQWTGSPSSMSASLGRVITTCRASQDINSYLSWFOQKPKKSPKTLIYRANRLVDGVPS 60

Cy 61 RFSGSGSGDYTLTISLQPEDFATYYCLOYDEFPYTFGGTKYIK 107
Db 61 RFSGSGSGDYTLTISLQYEDFGIYYCCQYDPSPTFGGTXLEIK 107

RESULT 5
US-08-472-788A-27
; Sequence 27, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TEXT:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-472-788A-27

Query Match      89.5%; Score 502; DB 1; Length 107;
Best Local Similarity 88.8%; Pred. No. 2.6e-43;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Cy 1 DIQWTGSPSSLSASVGDRTVITCKASQDINSYLSWFOQKPKAKPTLIYRANRLVDGVPS 60
Db 1 DIQWTGSPSSMSASLGRVITTCRASQDINSYLSWFOQKPKKSPKTLIYRANRLVDGVPS 60

Cy 61 RFSGSGSGDYTLTISLQPEDFATYYCLOYDEFPYTFGGTKYIK 107
Db 61 RFSGSGSGDYTLTISLQYEDFGIYYCCQYDPSPTFGGTXLEIK 107

RESULT 6
US-08-477-531B-27
; Sequence 27, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-531B-27
```

Query Match 89.5%; Score 502; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 2.6e-43;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVITTCRASQDINSYLSWFOQKPGKAPKTIYRANRLVDGVPS 60
DB 1 DIQMTQSPSSLSASVDGVITTCRASQDINSYLSWFOQKPGKAPKTIYRANRLVDGVPS 60
QY 61 RFGSGSGQDYTLTISLOPEDFATYYCLOVDEFPYTFGGGTKEIK 107
DB 61 RFGSGSGQDYTLTISLOPEDFATYYCLOVDEFPYTFGGGTKEIK 107

RESULT 7

US-08-082-842A-27
Sequence 27, Application US/08082842A
Patent No. 5869619
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kesseler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/082, 842A
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842A-27

Query Match 89.5%; Score 502; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 2.6e-43;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVITTCRASQDINSYLSWFOQKPGKAPKTIYRANRLVDGVPS 60
DB 1 DIQMTQSPSSLSASVDGVITTCRASQDINSYLSWFOQKPGKAPKTIYRANRLVDGVPS 60
QY 61 RFGSGSGQDYTLTISLOPEDFATYYCLOVDEFPYTFGGGTKEIK 107
DB 61 RFGSGSGQDYTLTISLOPEDFATYYCLOVDEFPYTFGGGTKEIK 107

RESULT 8

US-09-647-468-107
Sequence 107, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHITO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
FILE REFERENCE: 053466/0289
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 107
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding of version "b1" of humanized L
US-09-647-468-107

Query Match 88.9%; Score 499; DB 4; Length 107;
Best Local Similarity 89.7%; Pred. No. 5.3e-43;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVITTCRASQDINSYLSWFOQKPGKAPKTIYRANRLVDGVPS 60
DB 1 DIQMTQSPSSLSASVDGVITTCRASQDINSYLSWFOQKPGKAPKTIYRANRLVDGVPS 60
QY 61 RFGSGSGQDYTLTISLOPEDFATYYCLOVDEFPYTFGGGTKEIK 107
DB 61 RFGSGSGQDYTLTISLOPEDFATYYCLOVDEFPYTFGGGTKEIK 107

RESULT 9
US-09-647-468-182
Sequence 182, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHITO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
FILE REFERENCE: 053466/0289
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 182
LENGTH: 127
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding of version "b1" of humanized L
US-09-647-468-182

Query Match 88.9%; Score 499; DB 4; Length 127;
Best Local Similarity 89.7%; Pred. No. 5.3e-43;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;


```

Qy 1 DIQMTPSSSLASVAGDRVTITCKASODINSYLSWFOOKPGKAPRTLIYRANRLVDGVP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 DIQMTPSSSLASVAGDRVTITCKASODIKSLSWFOOKPGKSPPTLIYATSLADGVP 80
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 RPSGSGSQDYTLTITSLQPEDFATYYCQLQYDEPFYTGCGTKVEIK 107
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 RPSGSGSQDYTLTITSLQPEDFATYYCQLQHGESPYTGCGTKVEIK 127
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
US-08-425-336-125
Sequence 125, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studzinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425.336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-425-336-125

Query Match 88.8%; Score 498; DB 1; Length 107;
Best Local Similarity 89.7%; Pred. No. 6.7e-43;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0

Qy 1 DIQMTPSSSLASVAGDRVTITCKASODINSYLSWFOOKPGKAPRTLIYRANRLVDGVP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQMTPSSSLASVAGDRVTITCRASODINSYLSWFOOKPGKAPRTLIYRANRLVDGVP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 RPSGSGSQDYTLTITSLQPEDFATYYCQLQYDEPFYTGCGTKVEIK 107
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RPSGSGSQDYTLTITSLQYEDFGLIYCOQYDESWPTGCGTKVEIK 107
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

US-08-488-113B-125
/ Sequence 125 Application US/08488113B
/ Patent No. 5744580
/ GENERAL INFORMATION:
/ APPLICANT: Better, Marc D.
/ APPLICANT: Carroll, Stephen F.
/ APPLICANT: Studilka, Gary M.
/ TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
/ TITLE OF INVENTION: Proteins
/ NUMBER OF SEQUENCES: 169
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McAndrews, Held & Malloy, Ltd.
/ STREET: 500 West Madison Street, 34th floor
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60661
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,113B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/425,336
/ FILING DATE: 18-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 125:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-488-113B-125

Query Match 88.8%; Score 498; DB 1; Length 107;
Best Local Similarity 89.7%; Pred. No. 6,7e-43;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSISASVGRVTTTCASODINSYLSWFOQPKGAKDKTIIYRANRLVDGVP 60
DB 1 DIQWTQSPSSISASVGRVTTTCASODINSYLSWFOQPKGAKDKTIIYRANRLSGLVP 60
QY 61 RFSSGGSGODYTLTSSLOPEDFATYYCLOYDEPPTFGGCTKXKIR 107
DB 61 RFSSGGSGDYTLTSSLOPEDFATYYCLOYDEPPTFGGCTKXKIR 107
QY 61 RFSSGGSGDYTLTSSLOPEDFATYYCLOYDEPPTFGGCTKXKIR 107
DB 61 RFSSGGSGDYTLTSSLOPEDFATYYCLOYDEPPTFGGCTKXKIR 107

```

RESULT 12

US-08-477-484B-125
; Sequence 125, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-484B-125

Query Match 88.8%; Score 498; DB 1; Length 107;
Best Local Similarity 89.7%; Pred. No. 6.7e-43;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYISWFOQKRGKAPKTLIRANFLVDGVS 60
DB 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYISWFOQKRGKAPKTLIRANFLVDGVS 60
QY 61 RFSGSGSGDTYTLTISLQPEDPATYVCLOYDEFFPYTFGGGTVEIK 107
DB 61 RFSGSGSGDTYTLTISLQPEDPATYVCLOYDEFFPYTFGGGTVEIK 107

RESULT 13

US-08-107-669D-65
; Sequence 65, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbalia
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2540
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-107-669D-65

Query Match 88.8%; Score 498; DB 1; Length 107;
Best Local Similarity 89.7%; Pred. No. 6.7e-43;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYISWFOQKRGKAPKTLIRANFLVDGVS 60
DB 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYISWFOQKRGKAPKTLIRANFLVDGVS 60
QY 61 RFSGSGSGDTYTLTISLQPEDPATYVCLOYDEFFPYTFGGGTVEIK 107
DB 61 RFSGSGSGDTYTLTISLQPEDPATYVCLOYDEFFPYTFGGGTVEIK 107

RESULT 14

US-08-472-788A-87
; Sequence 87, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbal, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-472-788A-87

Query Match      88.8%; Score 498; DB 1; Length 107;
Best Local Similarity 89.7%; Pred. No. 6.7e-43;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAKTIIYRANRLVDCVPS 60
   |||||
DB 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAKTIIYRANRLVDCVPS 60
   |||||

QY 61 RFSGSGSGDPTLTITSLQPEDPATYCYCQYDEFPYFGGSKVEIK 107
   |||||
DB 61 RFSGSGSGDPTLTITSLQYBDFGIYCCQYDSESPWTFGGSKVEIK 107
   |||||

RESULT 15
; US-08-477-531B-65
; Sequence 65, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
```

```
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbal
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-531B-65

Query Match      88.8%; Score 498; DB 2; Length 107;
Best Local Similarity 89.7%; Pred. No. 6.7e-43;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAKTIIYRANRLVDCVPS 60
   |||||
DB 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAKTIIYRANRLVDCVPS 60
   |||||

QY 61 RFSGSGSGDPTLTITSLQPEDPATYCYCQYDEFPYFGGSKVEIK 107
   |||||
DB 61 RFSGSGSGDPTLTITSLQYBDFGIYCCQYDSESPWTFGGSKVEIK 107
   |||||

Search completed: December 29, 2004, 18:09:14
Job time : 19.4646 secs
```

THIS IS A BLANK (USP)

;; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;; FILE REFERENCE: 053466/0289
;; CURRENT APPLICATION NUMBER: US/09/647,468
;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: PCT/JP99/01768
;; PRIOR FILING DATE: 1999-04-02
;; PRIOR APPLICATION NUMBER: JP 10-91850
;; PRIOR FILING DATE: 1998-04-03
;; NUMBER OF SEQ ID NOS: 183
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 140
;; LENGTH: 118
;; TYPE: PRT
;; ORGANISM: Mus sp.
;; FEATURE:
;; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF
US-09-647-468-140

Query Match
Best Local Similarity 86.5%; Score 560.5; DB 4; Length 118;
Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLWIGYIDPYGDPGY 60
DB 1 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLWIGYIDPYGDPGY 60
QY 61 SOKFKGKATLTVDKSSSTAYMHLNLSITSDSAVYYCARGNFPYYFDYWGQGTLLTVSS 119
DB 61 NOKFKGKATLTVDKSSSTAYMHLNLSITSDSAVYYCARGGE-GYFDYWGQGTLLTVSS 118

RESULT 3
US-09-647-468-153
;; Sequence 153, Application US/09647468
;; Patent No 6677436
;; GENERAL INFORMATION:
;; APPLICANT: SATO, KOH
;; APPLICANT: ADACHI, HIDEKI
;; APPLICANT: YABUTA, NAOKIHO
;; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;; FILE REFERENCE: 053466/0289
;; CURRENT APPLICATION NUMBER: US/09/647,468
;; CURRENT FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: PCT/JP99/01768
;; PRIOR FILING DATE: 1999-04-02
;; PRIOR APPLICATION NUMBER: JP 10-91850
;; NUMBER OF SEQ ID NOS: 183
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 153
;; LENGTH: 137
;; TYPE: PRT
;; ORGANISM: Mus sp.
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;; OTHER INFORMATION: sequence coding for H chain V region of anti-TF
US-09-647-468-153

Query Match
Best Local Similarity 86.5%; Score 560.5; DB 4; Length 137;
Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLWIGYIDPYGDPGY 60
DB 20 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLWIGYIDPYGDPGY 79
QY 61 SOKFKGKATLTVDKSSSTAYMHLNLSITSDSAVYYCARGNFPYYFDYWGQGTLLTVSS 119
DB 80 NOKFKGKATLTVDKSSSTAYMHLNLSITSDSAVYYCARGGE-GYFDYWGQGTLLTVSS 137

RESULT 4
US-09-647-468-154
;; Sequence 154, Application US/09647468
;; Patent No. 6677436
;; GENERAL INFORMATION:
;; APPLICANT: SATO, KOH
;; APPLICANT: ADACHI, HIDEKI
;; APPLICANT: YABUTA, NAOKIHO
;; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;; FILE REFERENCE: 053466/0289
;; CURRENT APPLICATION NUMBER: US/09/647,468
;; CURRENT FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: PCT/JP99/01768
;; PRIOR FILING DATE: 1999-04-02
;; PRIOR APPLICATION NUMBER: JP 10-91850
;; NUMBER OF SEQ ID NOS: 183
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 154
;; LENGTH: 137
;; TYPE: PRT
;; ORGANISM: Mus sp.
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;; OTHER INFORMATION: sequence coding for H chain V region of anti-TF
US-09-647-468-154

Query Match
Best Local Similarity 86.5%; Score 560.5; DB 4; Length 137;
Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLWIGYIDPYGDPGY 60
DB 20 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLWIGYIDPYGDPGY 79
QY 61 SOKFKGKATLTVDKSSSTAYMHLNLSITSDSAVYYCARGNFPYYFDYWGQGTLLTVSS 119
DB 80 NOKFKGKATLTVDKSSSTAYMHLNLSITSDSAVYYCARGGE-GYFDYWGQGTLLTVSS 137

RESULT 5
US-08-273-146-55
;; Sequence 55, Application US/08273146
;; Patent No 5655885
;; GENERAL INFORMATION:
;; APPLICANT: Smith, Rodger
;; APPLICANT: McCafferty, John
;; APPLICANT: Chiswell, David
;; APPLICANT: Darzley, Michael J.
;; APPLICANT: Fitzgerald, Kevin
;; APPLICANT: Kenteen, John H.
;; APPLICANT: Martin, Mark T.
;; APPLICANT: Tiltmas, Richard C.
;; APPLICANT: Williams, Richard O.
;; TITLE OF INVENTION: The Isolation and Production of
;; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
;; NUMBER OF SEQUENCES: 71
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: IGEM, Inc.
;; STREET: 1530 East Jefferson St.
;; CITY: Rockville
;; STATE: MD
;; COUNTRY: USA
;; ZIP: 20852
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-11/D-27

Query Match 78.6%; Score 509.5; DB 1; Length 135;
Best Local Similarity 80.7%; Pred. No. 1e-41; Mismatches 96; Conservative 11; Indels 9; Gaps 3; Gaps 1;

QY 1 EIQLOOSGPELVKPGASVYKSCASGYAFTYNNMTWYKQSHGKSLWIGYIDPYGPGY 60
DB 20 EIQLOOSGPELVKPGASVYKSCASGYAFTYNNMTWYKQSHGKSLWIGYIDPYGPGY 79
QY 61 SQKFKGKATLVYDKSSSTAYMHNLSTSEDSAVYYCARGNFPYFDYWGQGLTVTYS 119
DB 80 NQKFKGKATLVYDKSSSTAYMHNLSTSEDSAVYYCARGN---RFAVWGQGLTVTYS 135

RESULT 9
US-08-436-717-27
Sequence 27, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-27

Query Match 78.6%; Score 509.5; DB 2; Length 135;
Best Local Similarity 80.7%; Pred. No. 1e-41; Mismatches 96; Conservative 11; Indels 9; Gaps 3; Gaps 1;

QY 1 EIQLOOSGPELVKPGASVYKSCASGYAFTYNNMTWYKQSHGKSLWIGYIDPYGPGY 60
DB 20 EIQLOOSGPELVKPGASVYKSCASGYAFTYNNMTWYKQSHGKSLWIGYIDPYGPGY 79
QY 61 SQKFKGKATLVYDKSSSTAYMHNLSTSEDSAVYYCARGNFPYFDYWGQGLTVTYS 119
DB 80 NQKFKGKATLVYDKSSSTAYMHNLSTSEDSAVYYCARGN---RFAVWGQGLTVTYS 135

RESULT 10
US-08-672-345C-105
Sequence 105, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry, Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-391-0525
TELEFAX: 212-278-0400
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-672-345C-105

Query Match 77.7%; Score 503.5; DB 2; Length 116;
Best Local Similarity 79.8%; Pred. No. 3.2e-41;

Matches 95; Conservative 11; Mismatches 10; Indels 3; Gaps 1;

QY 1 E10LQSGPELVKPGASVYKSCASGYAFNTNMYWVKOSHGKSLWIGYIDPYGPGY 60
 DB 1 E1H0QSGPELVKPGASVYKSCASGYAFNTNMYWVKOSHGKSLWIGYIDPYGPGY 60
 QY 61 S0KFKGKATLVVDSSTAVMHNLSTSEDSAVYYCARNGNFPYFDYWGQGTTLTVSS 119
 DB 61 N0KFKGKATLVVDSSTAVMHNLSTSEDSAVYYCARNGGL---FAYWKGTLTVTVA 116

RESULT 11

US-09-214-095D-90
 ; Sequence 90, Application US/09214095D
 ; Patent No. 6280987
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 51400-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/214,095D
 ; CURRENT FILING DATE: 1999-07-19
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 90
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-214-095D-90

Query Match 77.7%; Score 503.5; DB 3; Length 116;
 Best Local Similarity 79.8%; Pred. No. 3.2e-41;
 Matches 95; Conservative 11; Mismatches 10; Indels 3; Gaps 1;

QY 1 E10LQSGPELVKPGASVYKSCASGYAFNTNMYWVKOSHGKSLWIGYIDPYGPGY 60
 DB 1 E1H0QSGPELVKPGASVYKSCASGYAFNTNMYWVKOSHGKSLWIGYIDPYGPGY 60
 QY 61 S0KFKGKATLVVDSSTAVMHNLSTSEDSAVYYCARNGNFPYFDYWGQGTTLTVSS 119
 DB 61 N0KFKGKATLVVDSSTAVMHNLSTSEDSAVYYCARNGGL---FAYWKGTLTVTVA 116

RESULT 12

US-09-647-468-143
 ; Sequence 143, Application US/09647468
 ; Patent No. 6677436
 ; GENERAL INFORMATION:
 ; APPLICANT: SATO, KOH
 ; APPLICANT: ADACHI, HIDEKI
 ; APPLICANT: YABUTA, NAOHIRO
 ; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
 ; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
 ; FILE REFERENCE: 053466/0289
 ; CURRENT APPLICATION NUMBER: US/09/647,468
 ; CURRENT FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: PCT/JP99/01768
 ; PRIOR FILING DATE: 1999-04-02
 ; PRIOR APPLICATION NUMBER: JP 10-91850
 ; PRIOR FILING DATE: 1998-04-03
 ; NUMBER OF SEQ ID NOS: 183
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 143
 ; LENGTH: 118
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF mouse
 ; OTHER INFORMATION: monoclonal antibody ATR-7
 US-09-647-468-143

Query Match 77.7%; Score 503.5; DB 4; Length 118;
 Best Local Similarity 80.0%; Pred. No. 3.2e-41;
 Matches 96; Conservative 11; Mismatches 10; Indels 3; Gaps 2;

QY 1 E10LQSGPELVKPGASVYKSCASGYAFNTNMYWVKOSHGKSLWIGYIDPYGPGY 60
 DB 1 D10LQSGPELVKPGASVYKSCASGYAFNTNMYWVKOSHGKSLWIGYIDPYGPGY 60
 QY 61 S0KFKGKATLVVDSSTAVMHNLSTSEDSAVYYCARNGNFPYFDYWGQGTTLTVSS 119
 DB 61 N0KFKGKATLVVDSSTAVMHNLSTSEDSAVYYCAR--GFYYDYDCTWGGTTLTVTVA 118

RESULT 13

US-09-647-468-157
 ; Sequence 157, Application US/09647468
 ; Patent No. 6677436
 ; GENERAL INFORMATION:
 ; APPLICANT: SATO, KOH
 ; APPLICANT: ADACHI, HIDEKI
 ; APPLICANT: YABUTA, NAOHIRO
 ; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
 ; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
 ; FILE REFERENCE: 053466/0289
 ; CURRENT APPLICATION NUMBER: US/09/647,468
 ; CURRENT FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: PCT/JP99/01768
 ; PRIOR FILING DATE: 1999-04-02
 ; PRIOR APPLICATION NUMBER: JP 10-91850
 ; PRIOR FILING DATE: 1998-04-03
 ; NUMBER OF SEQ ID NOS: 183
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 157
 ; LENGTH: 137
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
 ; OTHER INFORMATION: sequence coding for H chain V region of anti-TF
 ; OTHER INFORMATION: mouse monoclonal antibody ATR-7
 US-09-647-468-157

Query Match 77.7%; Score 503.5; DB 4; Length 137;
 Best Local Similarity 80.0%; Pred. No. 3.9e-41;
 Matches 96; Conservative 11; Mismatches 10; Indels 3; Gaps 2;

QY 1 E10LQSGPELVKPGASVYKSCASGYAFNTNMYWVKOSHGKSLWIGYIDPYGPGY 60
 DB 20 D10LQSGPELVKPGASVYKSCASGYAFNTNMYWVKOSHGKSLWIGYIDPYGPGY 79
 QY 61 S0KFKGKATLVVDSSTAVMHNLSTSEDSAVYYCARNGNFPYFDYWGQGTTLTVSS 119
 DB 80 N0KFKGKATLVVDSSTAVMHNLSTSEDSAVYYCAR--GFYYDYDCTWGGTTLTVTVA 137

RESULT 14

US-08-672-345C-14
 ; Sequence 14, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C
 FILING DATE: 24-JUN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/51400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-672-345C-14

Query Match	76.9%	Score 498.5	DB 2	Length 116
Best Local Similarity	79.7%	Pred. No. 9.6e-41		
Matches 94	Conservative 10	Mismatches 11	Indels 3	Gaps 1

[illegible]

RESULT 15
 US-09-214-095D-14
 ; Sequence 14, Application US/09214095D
 ; Patent No. 6280987
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry, Donald
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; FILE REFERENCE: 51400-A-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/214,095D
 ; CURRENT FILING DATE: 1999-07-19
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: *Murinae* gen. sp.
 ; US-09-214-095D-14

Query Match	76.9%	Score 498.5	DB 3	Length 116
Best Local Similarity	79.7%	Pred. No. 9,6e-41		
Matches	94	Conservative 10	Mismatches 11	Indels 3
			Gaps	1
QY	1	ETQLQSQSPELVKPGASVYKSCAKGAYFTNTNTMYWVQSHKSLSEWTGYTDIPYDGDCY	60	
	::	::		
Db	1	DVQQLQESPELVKPGASVYKSCAKGAYFTNTNTMYWVQSHKSLSEWTGYTDIPYDGDCY	60	
	::	::		
QY	61	SOKEFGKATLTVDKSSSTAYMHNLSTSDSAVYYCARGNFPFYFDYDGGQDTLLVS	118	
	::	::		
Db	61	NQKEFGKATLTVDKSSSTAYMHNLSTSDSAVYYCARGGD---FAVWGGDTLLVS	115	

Search completed: December 29, 2004, 18:08:58
Job time : 22.5354 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 29, 2004, 17:47:08 ; Search time 20.5354 Seconds

(without alignments)
384.304 Million cell updates/sec

Title: US-10-774-076-12

Perfect score: 642
Sequence: 1 EYQVVGSGAEVKKPGASVKI.....GNPPYFDYWGCTVTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgnt2_6/prodata/1/1aa/5A COMB.pep.*
2: /cgnt2_6/prodata/1/1aa/5E COMB.pep.*
3: /cgnt2_6/prodata/1/1aa/6A COMB.pep.*
4: /cgnt2_6/prodata/1/1aa/6B COMB.pep.*
5: /cgnt2_6/prodata/1/1aa/6C COMB.pep.*
6: /cgnt2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	497.5	77.5	135	1 US-08-137-117D-102	Sequence 102, App
2	497.5	77.5	135	2 US-08-436-717-102	Sequence 102, App
3	496.5	77.3	116	2 US-08-561-521-41	Sequence 41, App1
4	496.5	77.3	116	5 PCT-US95-01219-41	Sequence 41, App1
5	491.5	76.6	135	1 US-08-137-117D-100	Sequence 100, App
6	491.5	76.6	135	2 US-08-436-717-100	Sequence 100, App
7	488.5	76.1	116	1 US-07-634-278-73	Sequence 73, App1
8	488.5	76.1	116	1 US-07-634-278-73	Sequence 73, App1
9	488.5	76.1	116	1 US-08-477-728-57	Sequence 57, App1
10	488.5	76.1	116	1 US-08-477-728-73	Sequence 73, App1
11	488.5	76.1	116	1 US-08-474-040-57	Sequence 57, App1
12	488.5	76.1	116	1 US-08-474-040-73	Sequence 73, App1
13	488.5	76.1	116	1 US-08-487-200-57	Sequence 57, App1
14	488.5	76.1	116	1 US-08-487-200-73	Sequence 73, App1
15	488.5	76.1	116	3 US-08-484-537-57	Sequence 57, App1
16	488.5	76.1	116	3 US-08-484-537-73	Sequence 73, App1
17	483.5	75.3	116	1 US-07-634-278-5	Sequence 5, App1
18	483.5	75.3	116	1 US-08-477-728-5	Sequence 5, App1
19	483.5	75.3	116	1 US-08-474-040-5	Sequence 5, App1
20	483.5	75.3	116	1 US-08-487-200-5	Sequence 5, App1
21	483.5	75.3	116	1 US-08-488-113B-169	Sequence 169, App
22	483.5	75.3	116	1 US-08-477-728-169	Sequence 169, App
23	483.5	75.3	116	1 US-08-107-669D-55	Sequence 55, App1
24	483.5	75.3	116	1 US-08-472-788A-86	Sequence 86, App1
25	483.5	75.3	116	2 US-08-477-531B-55	Sequence 55, App1
26	483.5	75.3	116	2 US-08-646-360-169	Sequence 169, App
27	483.5	75.3	116	2 US-08-082-842A-86	Sequence 86, App1

28	483.5	75.3	116	3 US-08-934-841-1	Sequence 1, App1
29	483.5	75.3	116	3 US-09-393-409-1	Sequence 1, App1
30	483.5	75.3	116	3 US-08-839-765-169	Sequence 169, App
31	483.5	75.3	116	3 US-09-136-389-169	Sequence 169, App
32	483.5	75.3	116	3 US-08-484-537-5	Sequence 5, App1
33	483.5	75.3	116	3 US-09-610-838-169	Sequence 169, App
34	483.5	75.3	116	4 US-09-711-485-169	Sequence 169, App
35	483.5	75.3	135	1 US-07-634-278-19	Sequence 19, App1
36	483.5	75.3	135	1 US-08-477-728-19	Sequence 19, App1
37	483.5	75.3	135	1 US-08-474-040-19	Sequence 19, App1
38	483.5	75.3	135	1 US-08-487-200-19	Sequence 19, App1
39	483.5	75.3	135	2 US-08-303-569B-31	Sequence 31, App1
40	483.5	75.3	135	3 US-08-484-537-7	Sequence 7, App1
41	483.5	75.3	139	4 US-09-355-925-7	Sequence 7, App1
42	483.5	75.3	139	4 US-09-355-925-8	Sequence 8, App1
43	483.5	75.3	139	4 US-09-269-921-125	Sequence 125, App
44	483.5	75.3	139	4 US-09-269-921-128	Sequence 128, App
45	483	75.2	117	3 US-08-525-539A-78	Sequence 78, App1

ALIGNMENTS

RESULT 1
US-08-137-117D-102
; Sequence 102, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masaaki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELETYPE: 904136
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-102

Query Match
Best Local Similarity 77.5%; Score 497.5; DB 1; Length 135;
Matches 94; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVOLVOSGAEVKKGASVYKISCKYSGYAFNTNMYRWQAPGKLEWIGYIDPYGDPGY 60
DB 20 QVQLVOSGAEVKKGASVYKISCKYSGYAFNTNMYRWQAPGKLEWIGYIDPYGDPGY 79
QY 61 SQRKGGATLTVDKSTAYMELSLRSEDTAVYYCARNGFPYFDYWGQGLTVTVSS 119
DB 80 NQKFKGVTMTVDSTNTAYMELSLRSEDTAVYYCARNGN--RFAVWGQGLTVTVSS 135

RESULT 2

US-08-436-717-102
Sequence 102, Application US/08436717
Patent No. 5817790

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993

APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399

TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-436-717-102

Query Match
Best Local Similarity 77.5%; Score 497.5; DB 2; Length 135;
Matches 94; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVOLVOSGAEVKKGASVYKISCKYSGYAFNTNMYRWQAPGKLEWIGYIDPYGDPGY 60
DB 20 QVQLVOSGAEVKKGASVYKISCKYSGYAFNTNMYRWQAPGKLEWIGYIDPYGDPGY 79
QY 61 SQRKGGATLTVDKSTAYMELSLRSEDTAVYYCARNGFPYFDYWGQGLTVTVSS 119
DB 80 NQKFKGVTMTVDSTNTAYMELSLRSEDTAVYYCARNGN--RFAVWGQGLTVTVSS 135

RESULT 3

US-08-561-521-41
Sequence 41, Application US/08561521
Patent No. 5840299

GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-41

Query Match
Best Local Similarity 77.3%; Score 496.5; DB 2; Length 116;
Matches 93; Conservative 12; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVOLVOSGAEVKKGASVYKISCKYSGYAFNTNMYRWQAPGKLEWIGYIDPYGDPGY 60
DB 1 QVQLVOSGAEVKKGASVYKISCKYSGYAFNTNMYRWQAPGKLEWIGYIDPYGDPGY 60
QY 61 SQRKGGATLTVDKSTAYMELSLRSEDTAVYYCARNGFPYFDYWGQGLTVTVSS 119
DB 61 NQKFKGVTMTVDSTNTAYMELSLRSEDTAVYYCARNGN--RFAVWGQGLTVTVSS 116

```

RESULT 4
PCT-US95-01219-41
; Sequence 41, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01219-41

Query Match 77.3%; Score 496.5; DB 5; Length 116;
Best Local Similarity 78.2%; Pred. No. 2,3e-40;
Matches 93; Conservative 12; Mismatches 11; Indels 3; Gaps 14

QY 1 EVQLVQSAEYVKKPPASVKISCKVGYAFTYNNMTVMYQAQPGKGLWIGYIDPYGDPGY 60
Db 1 QVQLVQSAEYVKKPPASVKYKSCKASGYFTSYIHVAQAQPGSLWVGWYIDPFNGISY 60
QY 61 SQPKGKATLTVDNSTAYNWLSSLRSEDPAYVYCARGNFPYFDYWGQGLTVTVSS 119
Db 61 NQKFGKATMTVDNSTAYNWLSSLRSEDPAYVYCARGN---RFAYWGQGLTVTVSS 116

RESULT 5
US-08-137-117D-100
; Sequence 100, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:

```

```

ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-100

Query Match          76.6%; Score 491.5; DB 1; Length 135;
Beet local similarity 77.3%; Pred. No. 8.1e-40;
Matches 92; Conservative 12; Mismatches 12; Indels 3; Gaps 1;

Qy      1 EVQLVDSAGAEVKKPGASVKISCKVSGYAFITNNMYWVRQAPGKGLIEWIGYIDIPYGDPGY 60
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      20 QVQLVDSAGAEVKRKGAIVNKSCKASGVSFYSIYTHWVRQAPGGGLEWVGVIDPFNGGSY 79
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy      61 SQRKSKATLLTDVKISTAYAMELSLRSEDTAVYYCARRGNFPIYPDIWGCGTLVTYSS 119
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      80 NQRKSKATLTVDSTNTAYAMELSLRSEDTACYCARGN---RFAYWGCGTLVTYSS 135
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 6
US-08-436-717-100
Sequence 100, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
```

```

? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/634,278
? FILING DATE: 19-DEC-1990
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/590,274
? FILING DATE: 28-SEP-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/310,252
? FILING DATE: 13-FEB-1989
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/290,975
? FILING DATE: 28-DEC-1988
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, William M.
? REGISTRATION NUMBER: 30,223
? REFERENCE/DOCKET NUMBER: 11823-002600
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 326-2400
? TELEFAX: (415) 326-2422
? INFORMATION FOR SEQ ID NO: 57:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 116 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
US-07-634-278-57

Query Match          76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2

QY      1 EVOLVQSGAEVVKPGASVKISCKVSGYAFITNYMMYMWQAQPGKLEWIGYIDPYGDEGY 60
DB      1 QVQLVQSGAEVVKPQESSKTVKSCAKSGYFTFTYNNMWQAQGGGLEWIGYIYPNGGIGY 60
QY      61 SOKPRGKATLVVDKSTSTAYVNEISLSRSEDTAIVYYCARGNFPYFYFDWGGGTLVTYSS 119
DB      61 NQKPKSKATLVADSESTNAYVNEISLSRSEDTAIVYYCAR--GRF-AMDYWGQGLVTYSS 116

RESULT 8
US-07-634-278-73
? Sequence 73, Application US/07634278
? Patent No. 5530101
? GENERAL INFORMATION:
? APPLICANT: QUEEN, Cary L.
? APPLICANT: CO, Man Sung
? APPLICANT: SCHNEIDER, William P.
? APPLICANT: LANDOLFI, Nicholas F.
? APPLICANT: COELINGH, Kathleen L.
? APPLICANT: SELICK, Harold E.
? TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
? NUMBER OF SEQUENCES: 113
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend Knourie and Crew
? STREET: 379 Lytton Avenue
? CITY: Palo Alto
? STATE: California
? COUNTRY: US
? ZIP: 94301
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/634,278
? FILING DATE: 19-DEC-1990
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-73

Query Match 76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLVSGAEVKKPKGASVKISCKVSGYAFPTNNMYVWRQAPGKLEWIGYIDPYGDPGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 QVOLVSGAEVKKPKGASVKISCKVSGYAFPTNNMYVWRQAPGKLEWIGYIDPYGDPGY 60
DB 61 SQFKKATLTVDKSTSTAMELSSLRSEPTAVTYCCARRGNFPYFDYWGQGLTVYSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 NQFKSKATTTADESTTAMELSSLRSEPTAVTYCCARRGNFPYFDYWGQGLTVYSS 116

RESULT 9

US-08-477-728-57
Sequence 57, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-57

Query Match 76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLVSGAEVKKPKGASVKISCKVSGYAFPTNNMYVWRQAPGKLEWIGYIDPYGDPGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 QVOLVSGAEVKKPKGASVKISCKVSGYAFPTNNMYVWRQAPGKLEWIGYIDPYGDPGY 60
DB 61 SQFKKATLTVDKSTSTAMELSSLRSEPTAVTYCCARRGNFPYFDYWGQGLTVYSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 NQFKSKATTTADESTTAMELSSLRSEPTAVTYCCARRGNFPYFDYWGQGLTVYSS 116

RESULT 10

US-08-477-728-73
Sequence 73, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-477-728-73

Query Match 76.1%; Score 488.5; DB 1; Length 116;
 Best Local Similarity 79.0%; Pred. No. 1.3e-39;
 Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVVLVSGAEVKKPGASVKISKVSGYAFNTNMTWVQAQPGKLEWIGYIDPYGDPGY 60
 DB 1 QVQLVSGAEVKKPGSSVKSVCKASGYFTDYNMHMTWQAQPGLEWIGYIYPNGGTGY 60
 QY 61 SQKPKGKATLTVDKSTAYMELSLRSEDTAVYYCARGNFPYFPYWGQGLTVTVSS 119
 DB 61 NQKFKSKATITADESTINAYMELSLRSEDTAVYYCAR--GRP-AMDYWGQGLTVTVSS 116

RESULT 11
 US-08-474-040-57
 Sequence 57, Application US/08474040
 Patent No. 5693761
 GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
 APPLICANT: CO, Man Sung
 APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas P.
 APPLICANT: COELINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,040
 FILING DATE: 07-JUN-1995

CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634,278
 FILING DATE: 19-DEC-1990
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-474-040-57

Query Match 76.1%; Score 488.5; DB 1; Length 116;
 Best Local Similarity 79.0%; Pred. No. 1.3e-39;
 Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVVLVSGAEVKKPGASVKISKVSGYAFNTNMTWVQAQPGKLEWIGYIDPYGDPGY 60
 DB 1 QVQLVSGAEVKKPGSSVKSVCKASGYFTDYNMHMTWQAQPGLEWIGYIYPNGGTGY 60
 QY 61 SQKPKGKATLTVDKSTAYMELSLRSEDTAVYYCARGNFPYFPYWGQGLTVTVSS 119
 DB 61 NQKFKSKATITADESTINAYMELSLRSEDTAVYYCAR--GRP-AMDYWGQGLTVTVSS 116

RESULT 12
 US-08-474-040-73
 Sequence 73, Application US/08474040
 Patent No. 5693761
 GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.
 APPLICANT: CO, Man Sung
 APPLICANT: SCHNEIDER, William P.
 APPLICANT: LANDOLFI, Nicholas P.
 APPLICANT: COELINGH, Kathleen L.
 APPLICANT: SELICK, Harold E.
 TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,040
 FILING DATE: 07-JUN-1995

CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/634,278
 FILING DATE: 19-DEC-1990
 APPLICATION NUMBER: US 07/590,274
 FILING DATE: 28-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/310,252
 FILING DATE: 13-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/290,975
 FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11823-002600
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-73

Query Match 76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLVSGAEVKKRGASVKISCKVSGYAFNNYNNWVROAPGKLEWIGYIDPYGDPGY 60
DB 1 QVQLVSGAEVKKRGSSVKVSKASGYTFDYNHNVROAPGQGLEWIGYIPYNGGTGY 60

QY 61 SQPKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARGNFPYFDYWGQGLTVYSS 119
DB 61 NQPKSKATTTADSTNTAYMELSLRSEDTAVYYCAR--GRP-AMDYWGQGLTVYSS 116

RESULT 13
US-08-487-200-57
Sequence 57, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-57

Query Match 76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLVSGAEVKKRGASVKISCKVSGYAFNNYNNWVROAPGKLEWIGYIDPYGDPGY 60
DB 1 QVQLVSGAEVKKRGSSVKVSKASGYTFDYNHNVROAPGQGLEWIGYIPYNGGTGY 60

QY 61 SQPKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARGNFPYFDYWGQGLTVYSS 119
DB 61 NQPKSKATTTADSTNTAYMELSLRSEDTAVYYCAR--GRP-AMDYWGQGLTVYSS 116

RESULT 14
US-08-487-200-73
Sequence 73, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-73

Query Match 76.1%; Score 488.5; DB 1; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-39;

Matches	94, Conservative	10, Mismatches	12, Indels	3, Gaps	2,
Qy	1	EVOLVOSAEYKRGASGYKISCKVSGVAFITNNYNNYNNQARCKGLEWIGYIDPYGDEGQ	60		
Dd	1	QVQLVDSGAEVKKRQSSIVSVCSKASGRTFTIDNNHWQAQEGGLEWIGYIFYPNGGCGY	60		
Qy	61	SOEKRGKATLVLDKSTSTAYNWEISLRSDEITAVNYCYCARGNFPYIFDYWGQGLTVYSS	119		
Dd	61	NQKSKSKKRTITADSTNTAINWELSLNSDEITAVNYCAR-GRP-AMDWGGGLTVYSS	116		

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:47:08 ; Search time 18.4646 Seconds
(without alignments)
384.304 Million cell updates/sec

Title: US-10-774-076-3

Perfect score: 563
Sequence: 1 DDKTQSPSSMYASISGERVT.....CLQYDERPYFGSGTKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgm2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgm2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgm2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgm2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgm2_6/ptodata/1/1aa/PTCUS.COMB.pep: *
6: /cgm2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	551	97.9	355	3	US-08-875-811-41 Sequence 41, Appl
2	551	97.9	355	3	US-08-875-811-49 Sequence 49, Appl
3	551	97.9	355	3	US-08-875-811-64 Sequence 64, Appl
4	551	97.9	358	3	US-08-875-811-45 Sequence 45, Appl
5	551	97.9	358	3	US-08-875-811-51 Sequence 51, Appl
6	551	97.9	360	3	US-08-875-811-47 Sequence 47, Appl
7	551	97.9	379	3	US-08-875-811-43 Sequence 43, Appl
8	546	97.0	127	3	US-08-348-548-4 Sequence 4, Appl
9	546	97.0	127	5	PCT-US95-15716-4 Sequence 26, Appl
10	541	96.1	107	1	US-08-107-669D-26 Sequence 26, Appl
11	541	96.1	107	1	US-08-472-788A-26 Sequence 26, Appl
12	541	96.1	107	2	US-08-477-531B-26 Sequence 26, Appl
13	541	96.1	107	2	US-08-082-842A-26 Sequence 26, Appl
14	531	94.3	107	1	US-08-425-336-123 Sequence 123, App
15	531	94.3	107	1	US-08-488-113B-123 Sequence 123, App
16	531	94.3	107	1	US-08-477-484B-123 Sequence 123, App
17	531	94.3	107	2	US-08-646-360-123 Sequence 123, App
18	531	94.3	107	3	US-08-839-765-123 Sequence 123, App
19	531	94.3	107	3	US-09-136-389-123 Sequence 123, App
20	531	94.3	107	3	US-09-610-838-123 Sequence 123, App
21	531	94.3	107	4	US-09-711-485-123 Sequence 123, App
22	527	93.6	107	2	US-08-290-592E-21 Sequence 21, Appl
23	527	93.6	107	5	PCT-US95-10053-18 Sequence 18, Appl
24	527	93.6	107	5	PCT-US96-09448-21 Sequence 8, Appl
25	525	92.7	142	2	US-08-737-129A-8 Sequence 2, Appl
26	522	92.7	142	2	US-08-579-940-2 Sequence 4, Appl
27	522	92.7	142	3	US-08-838-692-4 Sequence 4, Appl

28	519.5	92.3	129	2	US-08-860-174A-5 Sequence 5, Appl
29	519.5	92.3	258	2	US-08-860-174A-13 Sequence 13, Appl
30	508	90.2	107	1	US-08-107-669D-27 Sequence 27, Appl
31	508	90.2	107	1	US-08-472-788A-27 Sequence 27, Appl
32	508	90.2	107	2	US-08-477-531B-27 Sequence 27, Appl
33	508	90.2	107	2	US-08-082-842A-27 Sequence 27, Appl
34	487	86.5	107	1	US-08-425-336-125 Sequence 125, App
35	487	86.5	107	1	US-08-488-113B-125 Sequence 125, App
36	487	86.5	107	1	US-08-477-484B-125 Sequence 125, App
37	487	86.5	107	1	US-08-107-669D-65 Sequence 65, Appl
38	487	86.5	107	1	US-08-472-788A-65 Sequence 65, Appl
39	487	86.5	107	2	US-08-477-531B-65 Sequence 65, Appl
40	487	86.5	107	2	US-08-646-360-125 Sequence 125, App
41	487	86.5	107	2	US-08-082-842A-87 Sequence 87, Appl
42	487	86.5	107	3	US-08-839-765-125 Sequence 125, App
43	487	86.5	107	3	US-09-136-389-125 Sequence 125, App
44	487	86.5	107	3	US-09-610-838-125 Sequence 125, App
45	487	86.5	107	4	US-09-711-485-125 Sequence 125, App

ALIGNMENTS

RESULT 1
US-08-875-811-41
Sequence 41, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Luis
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02568
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-41
Query Match 97.9%; Score 551; DB 3; Length 355;
Best Local Similarity 97.2%; Pred. No. 8.4e-46;

Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDKMTQSSPMYASIGERVTITTCASQDINSYLSWFOQKRGKSPKTLIYRANRLVDGVPS 60
DB 1 DDKMTQSSPMYASIGERVTITTCASQDINSYLSWFOQKRGKSPKTLIYRANRLVDGVPS 60
QY 61 RFGSGSGQDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGTKEIK 107
DB 61 RFGSGSGQDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGTKEIK 107

RESULT 2

US-08-875-811-49
Sequence 49, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fairb, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-49

Query Match 97.9%; Score 551; DB 3; Length 355;
Best Local Similarity 97.2%; Pred. No. 8.4e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDKMTQSSPMYASIGERVTITTCASQDINSYLSWFOQKRGKSPKTLIYRANRLVDGVPS 60
DB 1 DDKMTQSSPMYASIGERVTITTCASQDINSYLSWFOQKRGKSPKTLIYRANRLVDGVPS 60
QY 61 RFGSGSGQDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGTKEIK 107
DB 61 RFGSGSGQDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGTKEIK 107

RESULT 3

US-08-875-811-64

Sequence 64, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fairb, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..355
OTHER INFORMATION: /note="B6PB[Met-(-1)]serTone"

Query Match 97.9%; Score 551; DB 3; Length 355;
Best Local Similarity 97.2%; Pred. No. 8.4e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDKMTQSSPMYASIGERVTITTCASQDINSYLSWFOQKRGKSPKTLIYRANRLVDGVPS 60
DB 1 DDKMTQSSPMYASIGERVTITTCASQDINSYLSWFOQKRGKSPKTLIYRANRLVDGVPS 60
QY 61 RFGSGSGQDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGTKEIK 107
DB 61 RFGSGSGQDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGTKEIK 107

RESULT 4

US-08-875-811-45
Sequence 45, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluís

APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-45

Query Match 97.9%; Score 551; DB 3; Length 358;
Best Local Similarity 97.2%; Pred. No. 8.5e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDKTQSPSSMYASLGRVYITTCASQDINSYISWFOCKPKSKPTLITYRANRLVDGVP 60
Db 119 DDKTQSPSSMYASLGRVYITTCASQDINSYISWFOCKPKSKPTLITYRANRLVDGVP 178

Qy 61 RFGSGSGQDYSLTISLSEYEDMGYYCLOYDEFPYFGGTTLEIK 107
Db 179 RFGSGSGQDYSLTISLSEYEDMGYYCLOYDEFPYFGGTTLEIK 225

RESULT 5
US-08-875-811-51
Sequence 51 Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Diane L.
APPLICANT: Bogue, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51

Query Match 97.9%; Score 551; DB 3; Length 358;
Best Local Similarity 97.2%; Pred. No. 8.5e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DDKTQSPSSMYASLGRVYITTCASQDINSYISWFOCKPKSKPTLITYRANRLVDGVP 60
Db 119 DDKTQSPSSMYASLGRVYITTCASQDINSYISWFOCKPKSKPTLITYRANRLVDGVP 178

Qy 61 RFGSGSGQDYSLTISLSEYEDMGYYCLOYDEFPYFGGTTLEIK 107
Db 179 RFGSGSGQDYSLTISLSEYEDMGYYCLOYDEFPYFGGTTLEIK 225

RESULT 6
US-08-875-811-47
Sequence 47 Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Diane L.
APPLICANT: Bogue, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51

FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-47

Query Match 97.9%; Score 551; DB 3; Length 360;
Best Local Similarity 97.2%; Pred. No. 8.5e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 121 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 180
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYLQYDEFPYTFGGTKLEIK 107
DB 181 RFSGSGSGQDYSLTISLSEYEDMGIIYCYLQYDEFPYTFGGTKLEIK 227

RESULT 7
US-08-875-811-43

Sequence 43, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02568
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-43

Query Match 97.9%; Score 551; DB 3; Length 379;
Best Local Similarity 97.2%; Pred. No. 9e-46;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 143 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 202
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYLQYDEFPYTFGGTKLEIK 107
DB 203 RFSGSGSGQDYSLTISLSEYEDMGIIYCYLQYDEFPYTFGGTKLEIK 249

RESULT 8
US-08-348-548-4

Sequence 4, Application US/08348548
Patent No. 6258529
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-548-4

Query Match 97.0%; Score 546; DB 3; Length 127;
Best Local Similarity 95.3%; Pred. No. 8.2e-46;
Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 21 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 80
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYLQYDEFPYTFGGTKLEIK 107
DB 81 RFSGSGSGQDYSLTISLSEYEDMGIIYCYLQYDEFPYTFGGTKLEIK 127

RESULT 9

PCT-US95-15716-4
; Sequence 4, Application PC/TUS9515716
; GENERAL INFORMATION:
; APPLICANT: Berdoz, Jose
; APPLICANT: Kraehenbuhl, Jean Pierre
; TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
; TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.308
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15716
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,548
; FILING DATE: 01-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06132/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-5070
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-15716-4

Query Match 97.0%; Score 546; DB 5; Length 127;
Best Local Similarity 95.3%; Pred. No. 8.2e-46;
Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDKTQSPSSMYASLGRVITTCASODINSYLSWFOOKPKGSKPTLIYRANRLVDGVP 60
Db 21 DDKTQSPSSMYASLGRVITTCASODINSYLSWFOOKPKGSKPTLIYRANRLVDGVP 80
QY 61 RFGSGSGGQDYSLTISLSLEYEDMGIIYCYDEFPYFGGCTKLEIK 107
Db 81 RFGSGSGGQDYSLTISLSLEYEDMGIIYCYDEFPYFGGCTKLEIK 127

RESULT 10
US-08-107-669D-26
; Sequence 26, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbalà
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-107-669D-26

Query Match 96.1%; Score 541; DB 1; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.1e-45;
Matches 109; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDKTQSPSSMYASLGRVITTCASODINSYLSWFOOKPKGSKPTLIYRANRLVDGVP 60
Db 1 DDKTQSPSSMYASLGRVITTCASODINSYLSWFOOKPKGSKPTLIYRANRLVDGVP 60
QY 61 RFGSGSGGQDYSLTISLSLEYEDMGIIYCYDEFPYFGGCTKLEIK 107
Db 61 RFGSGSGGQDYSLTISLSLEYEDMGIIYCYDEFPYFGGCTKLEIK 107

RESULT 11
US-08-472-788A-26
; Sequence 26, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalá, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-26

Query Match 96.1%; Score 541; DB 1; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.1e-45;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLTYRANRLVDGVPS 60
DB 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLTYRANRLVDGVPS 60
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYTFGGGTKLEIK 107
DB 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYTFGGGTKLEIK 107

RESULT 12

US-08-477-531B-26
Sequence 26, Application US/08477531B
Patent No. 5821123
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbalá
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-531B-26

Query Match 96.1%; Score 541; DB 2; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.1e-45;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLTYRANRLVDGVPS 60
DB 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLTYRANRLVDGVPS 60
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYTFGGGTKLEIK 107
DB 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYTFGGGTKLEIK 107

RESULT 13

US-08-082-842A-26
Sequence 26, Application US/08082842A
Patent No. 5869619
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,842A
FILING DATE: 23-JUN-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalá, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842A-26

Query Match 96.1%; Score 541; DB 2; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.1e-45;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLTYRANRLVDGVPS 60
DB 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLTYRANRLVDGVPS 60
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYTFGGGTKLEIK 107
DB 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYTFGGGTKLEIK 107

Db 61 RFGSGSGGDYSLTISLDEDMGIYCCQYDESPWTFGGGTLEIK 107

RESULT 14

US-08-425-336-123
; Sequence 123, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-336-123

Query Match 94.3%; Score 531; DB 1; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.9e-44;
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 1 DIRMTPSSSMVSLGRVITTCASODINSYLSWFOQKPKSLTIYRANRLVDSVPS 60
1 DIRMTPSSSMVSLGRVITTCASODINSYLSWFOQKPKSLTIYRANRLVDSVPS 60

QY 61 RFGSGSGGDYSLTISLDEDMGIYCCQYDESPWTFGGGTLEIK 107
Db 61 RFGSGSGGDYSLTISLDEDMGIYCCQYDESPWTFGGGTLEIK 107

RESULT 15
US-08-488-113B-123
; Sequence 123, Application US/08488113B
; Patent No. 5744580

GENERAL INFORMATION:

; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-123

Query Match 94.3%; Score 531; DB 1; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.9e-44;
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 1 DIRMTPSSSMVSLGRVITTCASODINSYLSWFOQKPKSLTIYRANRLVDSVPS 60
1 DIRMTPSSSMVSLGRVITTCASODINSYLSWFOQKPKSLTIYRANRLVDSVPS 60

QY 61 RFGSGSGGDYSLTISLDEDMGIYCCQYDESPWTFGGGTLEIK 107
Db 61 RFGSGSGGDYSLTISLDEDMGIYCCQYDESPWTFGGGTLEIK 107

Search completed: December 29, 2004, 18:08:59
Job time : 19.4646 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:47:08 / Search time 20.0177 Seconds
(without alignment)
384.304 Million cell updates/sec

Title: US-10-774-076-4

Perfect score: 617
Sequence: 1 EVGQSGAGELVRSGASVYL.....YGTITFAVWGQGLTVWSA 116

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
7: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*
8: /cgn2_6/ptodata/1/1aa/6E.COMB.pep:*
9: /cgn2_6/ptodata/1/1aa/6F.COMB.pep:*
10: /cgn2_6/ptodata/1/1aa/6G.COMB.pep:*
11: /cgn2_6/ptodata/1/1aa/6H.COMB.pep:*
12: /cgn2_6/ptodata/1/1aa/6I.COMB.pep:*
13: /cgn2_6/ptodata/1/1aa/6J.COMB.pep:*
14: /cgn2_6/ptodata/1/1aa/6K.COMB.pep:*
15: /cgn2_6/ptodata/1/1aa/6L.COMB.pep:*
16: /cgn2_6/ptodata/1/1aa/6M.COMB.pep:*
17: /cgn2_6/ptodata/1/1aa/6N.COMB.pep:*
18: /cgn2_6/ptodata/1/1aa/6O.COMB.pep:*
19: /cgn2_6/ptodata/1/1aa/6P.COMB.pep:*
20: /cgn2_6/ptodata/1/1aa/6Q.COMB.pep:*
21: /cgn2_6/ptodata/1/1aa/6R.COMB.pep:*
22: /cgn2_6/ptodata/1/1aa/6S.COMB.pep:*
23: /cgn2_6/ptodata/1/1aa/6T.COMB.pep:*
24: /cgn2_6/ptodata/1/1aa/6U.COMB.pep:*
25: /cgn2_6/ptodata/1/1aa/6V.COMB.pep:*
26: /cgn2_6/ptodata/1/1aa/6W.COMB.pep:*
27: /cgn2_6/ptodata/1/1aa/6X.COMB.pep:*
28: /cgn2_6/ptodata/1/1aa/6Y.COMB.pep:*
29: /cgn2_6/ptodata/1/1aa/6Z.COMB.pep:*
30: /cgn2_6/ptodata/1/1aa/6[.COMB.pep:*
31: /cgn2_6/ptodata/1/1aa/6].COMB.pep:*
32: /cgn2_6/ptodata/1/1aa/6^.COMB.pep:*
33: /cgn2_6/ptodata/1/1aa/6_.COMB.pep:*
34: /cgn2_6/ptodata/1/1aa/6+.COMB.pep:*
35: /cgn2_6/ptodata/1/1aa/6=.COMB.pep:*
36: /cgn2_6/ptodata/1/1aa/6,.COMB.pep:*
37: /cgn2_6/ptodata/1/1aa/6;.COMB.pep:*
38: /cgn2_6/ptodata/1/1aa/6:.COMB.pep:*
39: /cgn2_6/ptodata/1/1aa/6;.COMB.pep:*
40: /cgn2_6/ptodata/1/1aa/6;.COMB.pep:*
41: /cgn2_6/ptodata/1/1aa/6;.COMB.pep:*
42: /cgn2_6/ptodata/1/1aa/6;.COMB.pep:*
43: /cgn2_6/ptodata/1/1aa/6;.COMB.pep:*
44: /cgn2_6/ptodata/1/1aa/6;.COMB.pep:*
45: /cgn2_6/ptodata/1/1aa/6;.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523	84.8	118	3	US-08-767-128-22
2	516	83.6	535	3	US-08-983-035A-38
3	508	82.3	124	1	US-08-017-570-6
4	508	82.3	124	1	US-08-471-426-6
5	508	82.3	124	5	PCT-US94-01709-6
6	507	82.2	136	4	US-09-564-329A-11
7	507	82.2	136	4	US-09-663-620-11
8	507	82.2	136	4	US-09-855-632-11
9	505	81.8	281	3	US-09-423-439-44
10	505	81.8	642	3	US-09-423-439-26
11	505	81.8	666	3	US-09-423-439-51
12	503	81.5	124	1	US-08-017-570-4
13	503	81.5	124	1	US-08-471-426-4
14	503	81.5	124	5	PCT-US94-01709-4
15	502	81.4	255	3	US-09-171-945-19
16	502	81.4	270	2	US-08-652-507-2
17	501	81.2	553	2	US-08-661-052-16
18	501	81.2	553	3	US-09-188-082-16
19	501	81.2	553	3	US-09-364-088-16
20	501	81.2	553	3	US-09-102-716-16
21	500	81.0	136	5	US-08-348-548-8
22	500	81.0	136	5	PCT-US95-15716-8
23	498.5	80.8	254	2	US-08-792-824-4
24	498.5	80.8	254	2	US-08-792-824-4
25	498.5	80.8	254	2	US-08-792-824-10
26	498.5	80.8	254	2	US-08-792-824-13
27	496	80.4	124	3	US-09-672-609-1

28	496	80.4	124	4	US-09-025-403A-1	Sequence 1, Appli
29	495.5	80.3	119	4	US-09-649-063-11	Sequence 11, Appl
30	495.5	80.3	248	4	US-09-649-063-23	Sequence 23, Appl
31	493.5	80.0	136	1	US-08-024-253-2	Sequence 2, Appli
32	490.5	79.5	117	2	US-08-290-592B-18	Sequence 18, Appl
33	490.5	79.5	117	5	PCT-US95-10053-15	Sequence 15, Appl
34	490.5	79.5	117	5	PCT-US96-09448-18	Sequence 18, Appl
35	487	78.9	120	3	US-09-171-945-11	Sequence 11, Appl
36	483.5	78.4	125	2	US-08-561-521-44	Sequence 44, Appl
37	483.5	78.4	125	5	PCT-US95-01219-44	Sequence 44, Appl
38	477.5	77.4	117	4	US-09-647-468-141	Sequence 141, App
39	477.5	77.4	136	4	US-09-647-468-155	Sequence 155, App
40	477.5	77.3	118	2	US-08-232-081B-38	Sequence 38, Appl
41	476.5	77.2	136	3	US-08-646-265A-29	Sequence 29, Appl
42	473.5	76.7	123	2	US-08-561-521-9	Sequence 9, Appli
43	473.5	76.7	123	5	PCT-US95-01219-9	Sequence 9, Appli
44	470	76.2	137	3	US-08-836-561-31	Sequence 31, Appl
45	470	76.2	137	4	US-09-434-122-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-767-128-22
Sequence 22, Application US/08767128
Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYLLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GORELL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 611079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648,49USP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-767-128-22

Query Match 84.8%; Score 523; DB 3; Length 118;
Best Local Similarity 86.4%; Pred. No. 2.8e-46;
Matches 102; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 1 EVQLQSGAEIVSGASVKLSCTASGFNIDKYYIHMKORPEQGLEWIGCIPDENGDTREY 60
DB 1 EVQLQSGAEIVSGASVKLSCTASGFNIDKYYIHMKORPEQGLEWIGCIPDENGDTREY 60
QY 61 APNFGKATMTADTSSNTAVYLSLTSEDYAVYIC--YGGITTFAYWGQGLTVVSA 116
DB 61 APNFGKATMTADTSSNTAVYLSLTSEDYAVYICNPYGDAMDYWGQGLTVVSS 118

RESULT 2

US-08-983-035A-38
Sequence 38, Application US/08983035A
Patent No. 6326464

GENERAL INFORMATION:
APPLICANT: CONSELLER, EMMANUEL
BRACCO, LAURENT

TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
US8 THEROF

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:

ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP

STREET: 1300 I Street, NW
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983,035A
FILING DATE: 20-Feb-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/01111
FILING DATE: 17-JUL-1996

APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: Strauss, William L.

REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-08-983-035A-38

Query Match 83.6%; Score 516; DB 3; Length 535;
Best Local Similarity 84.7%; Pred. No. 9.1e-45;
Matches 100; Conservative 6; Mismatches 8; Indels 4; Gaps 2;

QY 1 EVQLQSGAEIVSGASVKLSCTASGFNIDKYYIHMKORPEQGLEWIGCIPDENGDTREY 60
DB 3 EVQLQSGAEIVSGASVKLSCTASGFNIDKYYIHMKORPEQGLEWIGCIPDENGDTREY 62
QY 61 APNFGKATMTADTSSNTAVYLSLTSEDYAVYIC--YGGITTFAYWGQGLTVVSA 116
DB 63 APNFGKATMTADTSSNTAVYLSLTSEDYAVYICNPYGDAMDYWGQGLTVVSS 118

RESULT 3

US-08-017-570-6
Sequence 6, Application US/08017570
Patent No. 5472693

GENERAL INFORMATION:
APPLICANT: GOURLE, BRIAN B

APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRIONIC
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer

STREET: P.O. Box 1967
CITY: Midland

STATE: MI
COUNTRY: US

ZIP: 48641-1967
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,570

FILING DATE: 19930216
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777

TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids
TYPE: AMINO ACID

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-017-570-6

Query Match 82.3%; Score 508; DB 1; Length 124;
Best Local Similarity 81.5%; Pred. No. 1e-44;
Matches 101; Conservative 4; Mismatches 11; Indels 8; Gaps 2;

QY 1 EVQLQSGAEIVSGASVKLSCTASGFNIDKYYIHMKORPEQGLEWIGCIPDENGDTREY 60
DB 1 EVQLQSGAEIVSGASVKLSCTASGFNIDKYYIHMKORPEQGLEWIGCIPDENGDTREY 60
QY 61 APNFGKATMTADTSSNTAVYLSLTSEDYAVYIC--YGGITTFAYWGQGLTV 112
DB 61 APNFGKATMTADTSSNTAVYLSLTSEDYAVYICNPYGDAMDYWGQGLTV 120

QY 113 TVSA 116
DB 121 TVSS 124

RESULT 4
US-08-471-426-6
Sequence 6, Application US/08471426
Patent No. 5808033
GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLON, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,426
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-426-6

Query Match 82.3%; Score 508; DB 1; Length 124;
Best Local Similarity 81.5%; Pred. No. 1e-44;
Matches 101; Conservative 4; Mismatches 11; Indels 8; Gaps 2;

Db 1 EVOLQSGAEIVRSGASVKTSGTASGNFKDYIHWKQREPGLEWIGCTIDPENGDTEY 60
QY 1 EVOLQSGAEIVRSGASVKTSGTASGNFKDYIHWKQREPGLEWIGCTIDPENGDTEY 60
Db 1 EVOLQSGAEIVRSGASVKTSGTASGNFKDYIHWKQREPGLEWIGCTIDPENGDTEY 60
QY 61 APNFGARATMTADSSNTAYVQLSLTSEDTAVYYC-----YGGTIT-----PAYNGGGTLY 112
Db 61 APKFGARATMTDTSSNTAYVQLSLTSEDTAVYYCNRGLSTMTITRPFVWGAGTTV 120
QY 113 TVSA 116
Db 121 TVSS 124

RESULT 5
PCT-US94-01709-6
Sequence 6, Application PC/TUS9401709
GENERAL INFORMATION:
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 38,777-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-01709-6

Query Match 82.3%; Score 508; DB 5; Length 124;
Best Local Similarity 81.5%; Pred. No. 1e-44;
Matches 101; Conservative 4; Mismatches 11; Indels 8; Gaps 2;

Db 1 EVOLQSGAEIVRSGASVKTSGTASGNFKDYIHWKQREPGLEWIGCTIDPENGDTEY 60
QY 1 EVOLQSGAEIVRSGASVKTSGTASGNFKDYIHWKQREPGLEWIGCTIDPENGDTEY 60
Db 1 EVOLQSGAEIVRSGASVKTSGTASGNFKDYIHWKQREPGLEWIGCTIDPENGDTEY 60
QY 61 APNFGARATMTADSSNTAYVQLSLTSEDTAVYYC-----YGGTIT-----PAYNGGGTLY 112
Db 61 APKFGARATMTDTSSNTAYVQLSLTSEDTAVYYCNRGLSTMTITRPFVWGAGTTV 120
QY 113 TVSA 116
Db 121 TVSS 124

RESULT 6
US-09-564-329A-11
Sequence 11, Application US/09564329A
Patent No. 6541212
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Safra, Douglas C.
TITLE OF INVENTION: BSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435,54US14
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261

```
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 09/203,939
/ PRIOR FILING DATE: 1998-12-02
/ PRIOR APPLICATION NUMBER: 09/251,835
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: 09/308,503
/ PRIOR FILING DATE: 1999-05-25
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: SCID Mice
US-09-564-329A-11
```

```
Query Match      82.2%; Score 507; DB 4; Length 136;
Best Local Similarity 84.5%; Pred. No. 1.5e-44;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
```

```
Qy      1 EVOLQSGAEIVRSGAVKLSCTASGFNIDKYYIHVKRPRGLEWIGICIDPENGDTRY 60
Db      14 EVOLQSGAEIVRSGAVKLSCTASGFNIDKYYIHVKRPRGLEWIGIDPENGDTRY 73
Qy      61 APNFGARATMTADTSNTAYLQSLTSEDTAVYYCYGGTITPAYWGQGLTVTVA 116
Db      74 VPKFGARATMTADTSNTAYLHLSLTSEDTAVYYCKTG---GFWGQGLTVTVA 125
```

```
RESULT 7
US-09-620-11
/ Sequence 11, Application US/09963620
/ Patent No. 6756036
/ GENERAL INFORMATION:
/ APPLICANT: Reiter, Robert E.
/ APPLICANT: Witte, Owen N.
/ APPLICANT: Saftan, Douglas C.
/ TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
/ FILE REFERENCE: 30435.54US14
/ CURRENT APPLICATION NUMBER: US/09/963,620
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 09/564,329
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: 09/359,326
/ PRIOR FILING DATE: 1999-07-20
/ PRIOR APPLICATION NUMBER: 08/814,279
/ PRIOR FILING DATE: 1997-03-10
/ PRIOR APPLICATION NUMBER: 60/071,141
/ PRIOR FILING DATE: 1998-01-12
/ PRIOR APPLICATION NUMBER: 60/074,675
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: 60/113,230
/ PRIOR FILING DATE: 1998-12-21
/ PRIOR APPLICATION NUMBER: 60/120,536
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: 60/124,658
/ PRIOR FILING DATE: 1999-03-16
/ PRIOR APPLICATION NUMBER: 09/038,261
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 09/203,939
/ PRIOR FILING DATE: 1998-12-02
/ PRIOR APPLICATION NUMBER: 09/251,835
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: 09/308,503
/ PRIOR FILING DATE: 1999-05-25
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: SCID Mice
US-09-963-620-11
```

```
Query Match      82.2%; Score 507; DB 4; Length 136;
```

```
Best Local Similarity 84.5%; Pred. No. 1.5e-44;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
Qy      1 EVOLQSGAEIVRSGAVKLSCTASGFNIDKYYIHVKRPRGLEWIGICIDPENGDTRY 60
Db      14 EVOLQSGAEIVRSGAVKLSCTASGFNIDKYYIHVKRPRGLEWIGIDPENGDTRY 73
Qy      61 APNFGARATMTADTSNTAYLQSLTSEDTAVYYCYGGTITPAYWGQGLTVTVA 116
Db      74 VPKFGARATMTADTSNTAYLHLSLTSEDTAVYYCKTG---GFWGQGLTVTVA 125
```

```
RESULT 8
US-09-855-632-11
/ Sequence 11, Application US/09855632
/ Patent No. 6790939
/ GENERAL INFORMATION:
/ APPLICANT: Reiter, Robert E.
/ APPLICANT: Witte, Owen N.
/ APPLICANT: Saftan, Douglas C.
/ TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
/ FILE REFERENCE: 30435.54US14
/ CURRENT APPLICATION NUMBER: US/09/855,632
/ PRIOR FILING DATE: 2001-05-14
/ PRIOR APPLICATION NUMBER: 09/564,329
/ PRIOR FILING DATE: 2000-05-03
/ PRIOR APPLICATION NUMBER: 09/359,326
/ PRIOR FILING DATE: 1999-07-20
/ PRIOR APPLICATION NUMBER: 08/814,279
/ PRIOR FILING DATE: 1997-03-10
/ PRIOR APPLICATION NUMBER: 60/071,141
/ PRIOR FILING DATE: 1998-01-12
/ PRIOR APPLICATION NUMBER: 60/074,675
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: 60/113,230
/ PRIOR FILING DATE: 1998-12-21
/ PRIOR APPLICATION NUMBER: 60/120,536
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: 60/124,658
/ PRIOR FILING DATE: 1999-03-16
/ PRIOR APPLICATION NUMBER: 09/038,261
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: 09/203,939
/ PRIOR FILING DATE: 1998-12-02
/ PRIOR APPLICATION NUMBER: 09/251,835
/ PRIOR FILING DATE: 1999-02-17
/ PRIOR APPLICATION NUMBER: 09/308,503
/ PRIOR FILING DATE: 1999-05-25
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: SCID Mice
US-09-855-632-11
```

```
Query Match      82.2%; Score 507; DB 4; Length 136;
Best Local Similarity 84.5%; Pred. No. 1.5e-44;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
Qy      1 EVOLQSGAEIVRSGAVKLSCTASGFNIDKYYIHVKRPRGLEWIGICIDPENGDTRY 60
Db      14 EVOLQSGAEIVRSGAVKLSCTASGFNIDKYYIHVKRPRGLEWIGIDPENGDTRY 73
Qy      61 APNFGARATMTADTSNTAYLQSLTSEDTAVYYCYGGTITPAYWGQGLTVTVA 116
Db      74 VPKFGARATMTADTSNTAYLHLSLTSEDTAVYYCKTG---GFWGQGLTVTVA 125
```

```
RESULT 9
US-09-423-439-44
/ Sequence 44, Application US/09423439
/ Patent No. 6339070
```

```

:
: GENERAL INFORMATION:
: APPLICANT: EMERY, Stephen Charles
: BLAXEY, David Charles
: TITLE OF INVENTION: CHEMICAL COMPOUNDS
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESSES:
: ADDRESS: Pillsbury Winthrop, L.L.P.
: STREET: 1100 New York Ave., N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/423,439
: FILING DATE: 09-NOV-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/GB98/01294
: FILING DATE: 05-MAY-1998
: APPLICATION NUMBER: GB 9709421.3
: FILING DATE: 10-MAY-1997
: INFORMATION FOR SEQ ID NO: 44:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 281 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-423-439-44

Query Match      81.8%; Score 505; DB 3; Length 281;
Best Local Similarity 80.8%; Pred. No. 5.6e-44;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

Cy 1 EVOLQSGAEIVRSGASVKTSGTASGFNIKDYIHWVKORPEQGLEWIGCIDPENGDTEY 60
    |||||
Db 23 EVOLQSGAEIVRSGASVKTSGTASGFNIKDYIHWVKORPEQGLEWIGCIDPENGDTEY 82
    |||||

Cy 61 APNFGKATMTADSSNTAYVQLSLTSEDTAVYYC---YGGITTFAYWGGTLVTVSA 116
    |||||
Db 83 APKRGKATLTADSSNTAYVQLSLTSEDTAVYYCHVLIYAGYLAIDYWGQGSVAVSS 142
    |||||

RESULT 10
US-09-423-439-26
: Sequence 26, Application US/09423439
: Patent No. 6339070
: GENERAL INFORMATION:
: APPLICANT: EMERY, Stephen Charles
: BLAXEY, David Charles
: TITLE OF INVENTION: CHEMICAL COMPOUNDS
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESSES:
: ADDRESS: Pillsbury Winthrop, L.L.P.
: STREET: 1100 New York Ave., N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/423,439
: FILING DATE: 09-NOV-1999
```

```

:
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/GB98/01294
: FILING DATE: 05-MAY-1998
: APPLICATION NUMBER: GB 9709421.3
: FILING DATE: 10-MAY-1997
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 642 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-423-439-26

Query Match      81.8%; Score 505; DB 3; Length 642;
Best Local Similarity 80.8%; Pred. No. 1.5e-43;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

Cy 1 EVOLQSGAEIVRSGASVKTSGTASGFNIKDYIHWVKORPEQGLEWIGCIDPENGDTEY 60
    |||||
Db 20 EVOLQSGAEIVRSGASVKTSGTASGFNIKDYIHWVKORPEQGLEWIGCIDPENGDTEY 79
    |||||

Cy 61 APNFGKATMTADSSNTAYVQLSLTSEDTAVYYC---YGGITTFAYWGGTLVTVSA 116
    |||||
Db 80 APKRGKATLTADSSNTAYVQLSLTSEDTAVYYCHVLIYAGYLAIDYWGQGSVAVSS 139
    |||||

RESULT 11
US-09-423-439-51
: Sequence 51, Application US/09423439
: Patent No. 6339070
: GENERAL INFORMATION:
: APPLICANT: EMERY, Stephen Charles
: BLAXEY, David Charles
: TITLE OF INVENTION: CHEMICAL COMPOUNDS
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESSES:
: ADDRESS: Pillsbury Winthrop, L.L.P.
: STREET: 1100 New York Ave., N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/423,439
: FILING DATE: 09-NOV-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/GB98/01294
: FILING DATE: 05-MAY-1998
: APPLICATION NUMBER: GB 9709421.3
: FILING DATE: 10-MAY-1997
: INFORMATION FOR SEQ ID NO: 51:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 666 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-423-439-51

Query Match      81.8%; Score 505; DB 3; Length 666;
Best Local Similarity 80.8%; Pred. No. 1.6e-43;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;
```

QY 1 EVOLQSGAEIVRSGASVYKLSCTASGFNIDYIHVWKORPEQGLEWIGCIDPENGDTEY 60
DB 20 EVOLQSGAEIVRSGASVYKLSCTASGFNIDYIHVWKORPEQGLEWIGCIDPENGDTEY 79
QY 61 APNFGRAITMTADSSNTAYIQLSSLTSEPTAVYYC-----YGGTIT-----FAWGGGTLV 116
DB 80 APKRGKATMTADSSNTAYIQLSSLTSEPTAVYYCCHVLIYAGVLANDVYGQGTSTAVSS 139

RESULT 12

US-08-017-570-4
Sequence 4, Application US/08017570
Patent No. 5472693

GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017.570
FILING DATE: 19930216
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-017-570-4

Query Match 81.5%; Score 503; DB 1; Length 124;
Best Local Similarity 80.6%; Pred. No. 3.4e-44;
Matches 100; Conservative 4; Mismatches 12; Indels 8; Gaps 2;

QY 1 EVOLQSGAEIVRSGASVYKLSCTASGFNIDYIHVWKORPEQGLEWIGCIDPENGDTEY 60
DB 1 EVOLQSGAEIVRSGASVYKLSCTASGFNIDYIHVWKORPEQGLEWIGCIDPENGDTEY 60
QY 61 APNFGRAITMTADSSNTAYIQLSSLTSEPTAVYYC-----YGGTIT-----FAWGGGTLV 112
DB 61 APKRGKATMTADSSNTAYIQLSSLTSEPTAVYYCCHVLIYAGVLANDVYGQGTSTAVSS 120
QY 113 TVSA 116
DB 121 AVSS 124

RESULT 13
US-08-471-426-4
Sequence 4, Application US/08471426
Patent No. 5808033

GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: MEZES, PETER S
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.426
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017.570
FILING DATE: 16-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-38,777
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-426-4

Query Match 81.5%; Score 503; DB 1; Length 124;
Best Local Similarity 80.6%; Pred. No. 3.4e-44;
Matches 100; Conservative 4; Mismatches 12; Indels 8; Gaps 2;

QY 1 EVOLQSGAEIVRSGASVYKLSCTASGFNIDYIHVWKORPEQGLEWIGCIDPENGDTEY 60
DB 1 EVOLQSGAEIVRSGASVYKLSCTASGFNIDYIHVWKORPEQGLEWIGCIDPENGDTEY 60
QY 61 APNFGRAITMTADSSNTAYIQLSSLTSEPTAVYYC-----YGGTIT-----FAWGGGTLV 112
DB 61 APKRGKATMTADSSNTAYIQLSSLTSEPTAVYYCCHVLIYAGVLANDVYGQGTSTAVSS 120
QY 113 TVSA 116
DB 121 AVSS 124

RESULT 14
PCT-US94-01709-4
Sequence 4, Application PC/TU9401709
GENERAL INFORMATION:
APPLICANT: THE DOW CHEMICAL COMPANY
APPLICANT: U.S.A. DEPT. OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI

COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01709
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: 36,777-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-01709-4

Query Match 81.5%; Score 503; DB 5; Length 124;

Best Local Similarity 80.6%; Pred. No. 3,4e-44;
Matches 100; Conservative 4; Mismatches 12; Indels 8; Gaps 2;

QY 1 EVQLQSGAEIVRSGASVYKLSCTASGFNIDKYYIMHWKQRPQGLEWIGCIDPENGDTEY 60
DB 1 EVQLQSGAEIVRSGASVYKLSCTASGFNIDKYYIMHWKQRPQGLEWIGCIDPENGDTEY 60
QY 61 APNFGKATMTADTSSNTAYVQLSSLTSEDTAVVYC---YGGTIT---PAYWGQGLTV 112
DB 61 APKFGKATMTDTSSTAYVQLSSLTSEDTAVVYCNRGLSTWITRMFDVWGAGCTTV 120
QY 113 TVSA 116
DB 121 AVSS 124

RESULT 15

US-09-171-945-19

Sequence 19, Application US/09171945

Patent No. 6277599

GENERAL INFORMATION:

APPLICANT: Emery, Stephen

APPLICANT: Copley, Clive Graham

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said

TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System

FILE REFERENCE: Monoclonal Antibody to CEA

CURRENT APPLICATION NUMBER: US/09171,945

CURRENT FILING DATE: 1998-10-29

PRIOR APPLICATION NUMBER: GB9703103.3

PRIOR FILING DATE: 1997-02-14

PRIOR APPLICATION NUMBER: GB9609405.7

PRIOR FILING DATE: 1996-05-04

PRIOR APPLICATION NUMBER: PCT/GB97/01165

PRIOR FILING DATE: 1997-04-29

NUMBER OF SEQ ID NOS: 131

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 255

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-19

Query Match 81.4%; Score 502; DB 3; Length 255;
Best Local Similarity 80.0%; Pred. No. 1e-43;

Matches 96; Conservative 8; Mismatches 12; Indels 4; Gaps 1;
QY 1 EVQLQSGAEIVRSGASVYKLSCTASGFNIDKYYIMHWKQRPQGLEWIGCIDPENGDTEY 60
DB 20 EVQLQSGAEIVRSGASVYKLSCTASGFNIDKYYIMHWKQRPQGLEWIGCIDPENGDTEY 79
QY 61 APNFGKATMTADTSSNTAYVQLSSLTSEDTAVVYC---YGGTITPAYWGQGLTVTSA 116
DB 80 APKFGKATMTDTSSTAYVQLSSLTSEDTAVVYCNRGLSTWITRMFDVWGAGCTTV 139

Search completed: December 29, 2004, 18:09:10
Job time : 31.0177 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:47:08 ; Search time 18,9823 Seconds
(without alignments)
384,304 Million cell updates/sec

Title: US-10-774-076-5

Perfect score: 576
Sequence: 1 QAVVTQESALTSPGERTVTL.....ALWYSHNHWFGGKTLTVLG 110

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgm2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgm2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgm2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgm2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgm2_6/ptodata/1/1aa/PTUS.COMB.pep: *
6: /cgm2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	97.0	112	3	US-09-157-370-6
2	559	97.0	269	2	US-08-428-257A-72
3	559	97.0	269	2	US-08-491-988-3
4	559	97.0	402	2	US-08-491-988-9
5	559	97.0	415	2	US-08-491-988-7
6	559	97.0	435	2	US-08-491-988-5
7	548	95.1	128	5	US-08-348-548-2
8	548	95.1	128	5	PCT-US95-15716-2
9	530.5	92.1	109	4	US-09-865-483-7
10	528	91.7	110	1	US-08-132-546-14
11	528	91.7	110	2	US-08-764-938-14
12	528	91.7	110	3	US-09-131-052-14
13	520	91.7	110	3	US-09-131-053A-14
14	520	90.3	106	2	US-08-440-354-2
15	520	90.3	106	2	US-08-463-087-2
16	517	89.8	109	2	US-08-672-345C-1
17	517	89.8	109	3	US-08-214-095D-1
18	513	89.1	109	2	US-08-672-345C-2
19	513	89.1	109	3	US-09-214-095D-2
20	509	88.4	115	6	5215889-3
21	504	87.5	109	2	US-08-672-345C-3
22	504	87.5	109	3	US-09-214-095D-3
23	504	87.5	109	3	US-09-214-095D-121
24	502	87.2	109	2	US-08-672-345C-93
25	476	82.6	109	2	US-08-672-345C-4
26	473	82.1	99	2	US-08-672-345C-91
27	473	82.1	99	3	US-09-214-095D-92

28	469	81.4	99	3	US-09-214-095D-88	Sequence 88, Appl
29	462	80.2	200	6	5189147-10	Patent No. 5189147
30	450.5	78.2	99	2	US-08-672-345C-92	Sequence 92, Appl
31	428	74.3	100	3	US-09-214-095D-96	Sequence 96, Appl
32	426	74.0	99	2	US-08-672-345C-94	Sequence 94, Appl
33	413.5	71.8	98	3	US-09-214-095D-4	Sequence 4, Appl
34	343.5	59.6	73	4	US-09-050-8618-5	Sequence 5, Appl
35	329	57.1	64	2	US-08-765-1798-23	Sequence 23, Appl
36	329	57.1	108	3	US-09-240-274-51	Sequence 51, Appl
37	329	57.1	108	3	US-09-240-274-52	Sequence 52, Appl
38	329	57.1	108	3	US-09-240-274-166	Sequence 166, Appl
39	316.5	54.9	240	3	US-09-049-672A-11	Sequence 11, Appl
40	315	54.7	108	3	US-09-240-274-53	Sequence 53, Appl
41	309	53.6	216	4	US-09-291-399A-8	Sequence 8, Appl
42	300	52.1	84	4	US-09-135-238B-5	Sequence 5, Appl
43	277	48.1	216	4	US-09-291-399A-10	Sequence 10, Appl
44	265.5	46.1	217	4	US-09-291-399A-7	Sequence 7, Appl
45	252	43.8	112	2	US-08-665-202-39	Sequence 39, Appl

ALIGNMENTS

```
RESULT 1
US-09-157-370-6
; Sequence 6, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEINBACHER, Boris
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157,370A
; EARLIER FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-157-370-6

Query Match          97.0%; Score 559; DB 3; Length 112;
Best Local Similarity 97.3%; Pred. No. 1.3e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 QAVVTQESALTSPGERTVTLTCRSSGTAVTTSNANVQKPKPLFTGLIGTINRVGV 60
Db 1 QAVVTQESALTSPGERTVTLTCRSSGTAVTTSNANVQKPKPLFTGLIGTINRVGV 60

Cy 61 PARFSGSLIDKALITTTGAQTDEDAIYFCALWYSHNHWFGGKTLTVLG 110
Db 61 PARFSGSLIDKALITTTGAQTDEDAIYFCALWYSHNHWFGGKTLTVLG 110

RESULT 2
US-08-428-257A-72
; Sequence 72, Application US/08428257A
; Patent No. 5865808
; GENERAL INFORMATION:
; APPLICANT: Spooner, Robert A.
; TITLE OF INVENTION: Compounds to target cells
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jules E. Goldberg
; STREET: 261 Madison Avenue
```

CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,257A
FILING DATE: 07/05/95
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-257A-72

Query Match 97.0%; Score 559; DB 2; Length 269;
Best Local Similarity 97.3%; Pred. No. 3,6e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QAVTQESALTSPGRTVTLTCRSSGAVTTSNSANWVQEKPDHFTGLIGGTINRPAV 60
DB 158 QAVTQESALTSPGRTVTLTCRSSGAVTTSNSANWVQEKPDHFTGLIGGTINRPAV 217
QY 61 PARFSGSLIDKKAALTITGAQTEDEAIFCALWYSNHWVFGGDTLTVLG 110
DB 218 PARFSGSLIDKKAALTITGAQTEDEAIFCALWYSNHWVFGGDTLTVLG 267

RESULT 3
US-08-491-988-3
Sequence 3, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPINETOS, AGAMENON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-3

Query Match 97.0%; Score 559; DB 2; Length 269;
Best Local Similarity 97.3%; Pred. No. 3,6e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QAVTQESALTSPGRTVTLTCRSSGAVTTSNSANWVQEKPDHFTGLIGGTINRPAV 60
DB 158 QAVTQESALTSPGRTVTLTCRSSGAVTTSNSANWVQEKPDHFTGLIGGTINRPAV 217
QY 61 PARFSGSLIDKKAALTITGAQTEDEAIFCALWYSNHWVFGGDTLTVLG 110
DB 218 PARFSGSLIDKKAALTITGAQTEDEAIFCALWYSNHWVFGGDTLTVLG 267

RESULT 4
US-08-491-988-9
Sequence 9, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPINETOS, AGAMENON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-9

Query Match 97.0%; Score 559; DB 2; Length 402;
Best Local Similarity 97.3%; Pred. No. 5,7e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QAVTQESALTSPGRTVTLTCRSSGAVTTSNSANWVQEKPDHFTGLIGGTINRPAV 60
DB 158 QAVTQESALTSPGRTVTLTCRSSGAVTTSNSANWVQEKPDHFTGLIGGTINRPAV 217
QY 61 PARFSGSLIDKKAALTITGAQTEDEAIFCALWYSNHWVFGGDTLTVLG 110
DB 218 PARFSGSLIDKKAALTITGAQTEDEAIFCALWYSNHWVFGGDTLTVLG 267

RESULT 5
US-08-491-988-7
Sequence 7, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPINETOS, AGAMENON A.

APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-7

Query Match 97.0%; Score 559; DB 2; Length 415;
Best Local Similarity 97.3%; Pred. No. 5.9e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QAVVTQSSALTTSGEIVTLTCRSTGAVTTSNANWQKPDHFTGLIGGTINRPGV 60
Db 158 QAVVTQSSALTTSGEIVTLTCRSTGAVTTSNANWQKPDHFTGLIGGTINRAGV 217
Qy 61 PARFSGSLIDGKALTTTGAQTEDEALYFCALWYSNHWFGGGTKLTVLG 110
Db 218 PARFSGSLIDGKALTTTGAQTEDEALYFCALWYSNHWFGGGTKLTVLG 267

RESULT 6
US-08-491-988-5
Sequence 5, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-5

Query Match 97.0%; Score 559; DB 2; Length 435;
Best Local Similarity 97.3%; Pred. No. 6.3e-48;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QAVVTQSSALTTSGEIVTLTCRSTGAVTTSNANWQKPDHFTGLIGGTINRPGV 60
Db 158 QAVVTQSSALTTSGEIVTLTCRSTGAVTTSNANWQKPDHFTGLIGGTINRAGV 217
Qy 61 PARFSGSLIDGKALTTTGAQTEDEALYFCALWYSNHWFGGGTKLTVLG 110
Db 218 PARFSGSLIDGKALTTTGAQTEDEALYFCALWYSNHWFGGGTKLTVLG 267

RESULT 7
US-08-348-548-2
Sequence 2, Application US/08348548
Patent No. 6258529
GENERAL INFORMATION:
APPLICANT: Beidoz, Jose
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-548-2

Query Match 95.1%; Score 548; DB 3; Length 128;
Best Local Similarity 96.3%; Pred. No. 1.9e-47;
Matches 105; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGTVTLTCRSSGTGAVTTSNANWQEKPDHLFTGLIGGTINRPGV 60
DB 20 QAVTQESALTTSPGTVTLTCRSSGTGAVTTSNANWQEKPDHLFTGLIGGTINRPGV 79
QY 61 PARFSGSLIGDKAALTTTGAQTEDEATYFCALWYSNHWVFGGKTLTVL 109
DB 80 PARFSGSLIGDKAALTTTGAQTEDEATYFCALWYSNHWVFGGKTLTVL 128

RESULT 8

PCT-US95-15716-2
Sequence 2, Application PC/TUS9515716
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
NUMBER OF SEQUENCES: 108
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15716
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-15716-2

Query Match 95.1%; Score 548; DB 5; Length 128;
Best Local Similarity 96.3%; Pred. No. 1.9e-47;
Matches 105; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGTVTLTCRSSGTGAVTTSNANWQEKPDHLFTGLIGGTINRPGV 60
DB 20 QAVTQESALTTSPGTVTLTCRSSGTGAVTTSNANWQEKPDHLFTGLIGGTINRPGV 79
QY 61 PARFSGSLIGDKAALTTTGAQTEDEATYFCALWYSNHWVFGGKTLTVL 109
DB 80 PARFSGSLIGDKAALTTTGAQTEDEATYFCALWYSNHWVFGGKTLTVL 128

RESULT 9

US-09-865-483-7
Sequence 7, Application US/09865483
GENERAL INFORMATION:
APPLICANT: Lee, Jong Wook et al.
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SU

FILE REFERENCE: 1599-0197P
CURRENT APPLICATION NUMBER: US/09/865,483
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 109
TYPE: PRT
ORGANISM: Escherichia coli
US-09-865-483-7

Query Match 92.1%; Score 530.5; DB 4; Length 109;
Best Local Similarity 93.6%; Pred. No. 8.9e-46;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 QAVTQESALTTSPGTVTLTCRSSGTGAVTTSNANWQEKPDHLFTGLIGGTINRPGV 60
DB 1 QAVTQESALTTSPGTVTLTCRSSGTGAVTTSNANWQEKPDHLFTGLIGGTINRPGV 60
QY 61 PARFSGSLIGDKAALTTTGAQTEDEATYFCALWYSNHWVFGGKTLTVL 110
DB 61 PARFSGSLIGDKAALTTTGAQTEDEATYFCALWYNNWVFGGKTLTVL 109

RESULT 10

US-08-122-546-14
Sequence 14, Application US/08122546
Patent No. 5591593
GENERAL INFORMATION:
APPLICANT: Courtenay-Luck, Nigel S
TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E Goldberg, Esq.
STREET: 261 Madison Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,546
FILING DATE: 09/29/93
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24,408
REFERENCE/DOCKET NUMBER: JG-EPC-1069PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 986-4090
TELEFAX: (212) 818-9479
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-122-546-14

Query Match 91.7%; Score 528; DB 1; Length 110;
Best Local Similarity 91.8%; Pred. No. 1.6e-45;
Matches 101; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGTVTLTCRSSGTGAVTTSNANWQEKPDHLFTGLIGGTINRPGV 60
DB 1 QAVTQESALTTSPGTVTLTCRSSGTGAVTTSNANWQEKPDHLFTGLIGGTINRPGV 60

```

QY      61 PARFSGSLGDKAALTITGAQTEDEALTYFCALMYSNHWFGGGTKLTVLG 110
        |||||
DB      61 PARFSGSLGDKAALTITGAQTEDEATYFCALMYSNHWFGGGTKLSRLG 110

```

RESULT 11
US-08-764-938-14
; Sequence 14, Application US/08764938
; Patent No. 5833943

1 GENERAL INFORMATION:
2 APPLICANT: Courtenay-Luck, Nigel S
3 TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
4 TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY
5 NUMBER OF SEQUENCES: 18
6 CORRESPONDENCE ADDRESS: 11

```

1
2
3 ADDRESS: Jules E Goldberg, Esq.
4 STREET: 261 Madison Avenue
5 CITY: New York
6 STATE: New York
7 COUNTRY: USA
8
9 ZIP: 10016
10
11 COMPUTER READABLE FORM:
12

```

```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,938
FILING DATE: December 13, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REFERENCE/DOCKET NUMBER: JG-EPC-1069PCT/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 986-4090
TELEFAX: (212) 818-9479
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-764-938-14

```

[illegible]

RESULT 12
 US-09-11-052-14
 : Sequence 14, Application US/0911052
 : Patent No. 6107469
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Courtenay-Luck, Nigel S
 :
 : TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
 :
 : NUMBER OF INVENTION: TANDDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY
 :
 : NUMBER OF SEQUENCES: 18
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Jules E Goldberg, Esq.
 :
 : STREET: 261 Madison Avenue
 :
 : CITY: New York
 :
 : STATE: New York
 :
 : COUNTRY: USA
 :
 : ZIP: 10016-2391
 :

```

;
;  COMPUTER READABLE FORM:
;
;  MEDIUM TYPE:  Floppy disk
;
;  COMPUTER:  IBM PC compatible
;
;  OPERATING SYSTEM:  PC-DOS/MS-DOS
;
;  SOFTWARE:  PatentIn Release #1.0, Version #1.25
;

```

```

? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/131,052
? FILING DATE: August 7, 1998
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Goldberg, Jules E
? REFERENCE/DOCKET NUMBER: JG-EPC-1069C-3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 986-4090
? TELEFAX: (212) 818-9479
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 110 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-09-131-052-14

Query Match          91.7%;   Score 528;   DB 3;   Length 110;
Best Local Similarity 91.8%;   Pred. No. 1.6e-45;
Matches 101; Conservative 2; Mismatches 7; Indels 0; Gaps 0

```

```

0Y      1 QAVVTOESALTTSPGETVLTLICRSSGTAVTSSANWQEKPHLPTGLIGTTIT
Db      1 QAVLTGFEALTTSPGEIVTLTLICRSSGTAVTSSVANWQEKPHLLTGLLGNTN
0Y      61 PARSSGLIDDKAALTTCGAQTDEPAIYFCALWYSNNHWVGCGTKLVLG 110
Db      61 PARSSGLIDDKAALTTCGAQTDEPAIYFCALWYSNNHWVGCGTKLSRLG 110

RESULT 13
US-09-131-053A-14
Sequence 14, Application US/09131053A
Patent No. 6174691
GENERAL INFORMATION:
APPLICANT: Courtenay-Luck, Nigel S
TITLE OF INVENTION: MINIMUM RECOGNITION UNIT OF PEM MUCIN
TITLE OF INVENTION: TANDEM REPEAT SPECIFIC MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Jules B Goldberg, Esq.
STREET: 261 Madison Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/131,053A
FILING DATE: August 7, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules B
REFERENCE/DOCKET NUMBER: JG-BPC-1069C-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 966-4090
TELEFAX: (212) 818-9479
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

```

US-09-131-053A-14

Query Match 91.7%; Score 528; DB 3; Length 110;
Best Local Similarity 91.8%; Pred. No. 1.6e-45;
Matches 101; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QAVVQESALTTSPGEVTLTCRSTGAVTTSNSANWVOEKPDHFTGLIGGTINRVPGV 60
DB 1 QAVVQESALTTSPGEVTLTCRSTGAVTTSNSANWVOEKPDHFTGLIGGTINRVPGV 60
QY 61 PARFSGSLIGDKKALTTTGAQTEDEALYFCALWYSNHWVFGGGTKLTVLG 110
DB 61 PARFSGSLIGDKKALTTTGAQTEDEALYFCALWYSNHWVFGGGTKLTVLG 110

RESULT 14

US-08-440-354-2
; Sequence 2, Application US/08440354
; Patent No. 5907034
; GENERAL INFORMATION:
; APPLICANT: Boblett, Klaus
; APPLICANT: Hermentin, Peter
; APPLICANT: Seemann, Gerhard
; TITLE OF INVENTION: A Monoclonal Antibody Against Complexed
; TITLE OF INVENTION: and No. 5907034Complexed Complexing Agents for Removing Heavy
; TITLE OF INVENTION: Metals from Aqueous Solutions and for Analysis
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSER: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,354
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,166
; FILING DATE: 02-FEB-1993
; APPLICATION NUMBER: US/07/664,789
; FILING DATE: 05-MAR-1991
; APPLICATION NUMBER: DE 4007079.4
; FILING DATE: 07-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavin Jr., Lawrence M.
; REGISTRATION NUMBER: 30,768
; REFERENCE/DOCKET NUMBER: HOAG-1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-440-354-2

Query Match 90.3%; Score 520; DB 2; Length 106;
Best Local Similarity 93.3%; Pred. No. 9.6e-45;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 VTQESALTTSPGEVTLTCRSTGAVTTSNSANWVOEKPDHFTGLIGGTINRVPGV 63
DB 2 VTQESALTTSPGEVTLTCRSTGAVTTSNSANWVOEKPDHFTGLIGGTINRVPGV 63

QY 64 FSGSLIGDKKALTTTGAQTEDEALYFCALWYSNHWVFGGGTKLTV 108
DB 62 FSGSLIGDKKALTTTGAQTEDEALYFCALWYSNHWVFGGGTKLTV 106

RESULT 15

US-08-463-087-2
; Sequence 2, Application US/08463087
; Patent No. 5908790
; GENERAL INFORMATION:
; APPLICANT: Boblett, Klaus
; APPLICANT: Hermentin, Peter
; APPLICANT: Seemann, Gerhard
; TITLE OF INVENTION: A Monoclonal Antibody Against Complexed
; TITLE OF INVENTION: and No. 5908790Complexed Complexing Agents for Removing Heavy
; TITLE OF INVENTION: Metals from Aqueous Solutions and for Analysis
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSER: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,087
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,789
; FILING DATE: 05-MAR-1991
; APPLICATION NUMBER: DE 4007079.4
; FILING DATE: 07-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavin Jr., Lawrence M.
; REGISTRATION NUMBER: 30,768
; REFERENCE/DOCKET NUMBER: HOAG-1043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-463-087-2

Query Match 90.3%; Score 520; DB 2; Length 106;
Best Local Similarity 93.3%; Pred. No. 9.6e-45;
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 VTQESALTTSPGEVTLTCRSTGAVTTSNSANWVOEKPDHFTGLIGGTINRVPGV 63
DB 2 VTQESALTTSPGEVTLTCRSTGAVTTSNSANWVOEKPDHFTGLIGGTINRVPGV 63
QY 64 FSGSLIGDKKALTTTGAQTEDEALYFCALWYSNHWVFGGGTKLTV 108
DB 62 FSGSLIGDKKALTTTGAQTEDEALYFCALWYSNHWVFGGGTKLTV 106

Search completed: December 29, 2004, 18:09:12
Job time : 20.9823 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 14.677 Seconds

(without alignments)
701.451 Million cell updates/sec

Title: US-10-774-076-14

Perfect score: 561

Sequence: 1 DIQWTQSPSSLSASVGDRTV.....CLOYDEPFYFGGKTVK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR_79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	86.6	127	2 S52447	Ig kappa chain V r
2	474	84.5	128	1 KVMST1	Ig kappa chain pre
3	470	83.8	234	2 S14237	Ig kappa chain pre
4	459	81.8	128	2 PLO101	Ig kappa chain pre
5	453	80.7	129	2 S52789	Ig kappa chain V r
6	452	80.6	125	2 S40333	Ig kappa chain V-J
7	451	80.4	107	2 S36264	Ig lambda chain V
8	451	80.4	108	2 B49047	Ig kappa chain V r
9	450	80.2	132	2 S40334	Ig kappa chain - h
10	449	80.0	129	2 S40369	Ig kappa chain - h
11	447	79.7	123	2 S40313	Ig kappa chain V-J
12	446	79.5	106	2 S20652	Ig kappa chain V r
13	444	79.1	108	1 K1H0U1	Ig kappa chain V-I
14	444	79.1	108	2 I39154	Ig kappa chain (BR
15	444	79.1	125	2 S40349	Ig kappa chain V-J
16	443	79.0	108	1 K1H0U1	Ig kappa chain V-I
17	442	78.8	108	1 K1H0U1	Ig kappa chain V-I
18	442	78.8	115	1 KVMST6	Ig kappa chain pre
19	442	78.8	123	2 S40331	Ig kappa chain - h
20	441	78.6	108	1 K1H0U1	Ig kappa chain V-I
21	440	78.4	108	2 S19674	Ig kappa chain V r
22	440	78.4	125	2 S40316	Ig kappa chain - h
23	439	78.3	107	2 I69017	anti-HIV envelope
24	439	78.3	108	1 K1H0U1	Ig kappa chain V-I
25	439	78.3	125	2 S40353	Ig kappa chain V-J
26	439	78.3	127	2 S40367	Ig kappa chain V-J
27	438	78.1	125	2 S40350	Ig kappa chain - h
28	436	77.7	104	2 S13700	Ig kappa chain V r
29	436	77.7	117	2 S46371	Ig kappa chain V-J

30	436	77.7	129	2 S40317	Ig kappa chain - h
31	435	77.7	129	2 S52793	Ig kappa chain V r
32	435	77.5	117	2 S46376	Ig kappa chain V-J
33	434	77.4	110	2 S44118	Ig kappa chain V-I
34	432	77.0	107	2 S36269	Ig lambda chain V
35	432	77.0	108	1 K1H0U1	Ig kappa chain V-I
36	432	77.0	141	2 A49134	Ig kappa chain V-I
37	430	76.6	98	2 P10655	Ig kappa chain V r
38	428	76.3	109	2 S31998	Ig kappa chain - h
39	428	76.3	131	2 S40352	Ig kappa chain V-J
40	427.5	76.2	107	1 K1H0U1	Ig kappa chain V-I
41	427	76.1	108	1 K1H0U1	Ig kappa chain V-I
42	427	76.1	108	1 K1H0U1	Ig kappa chain V-I
43	427	76.1	108	1 K1H0U1	Ig kappa chain V-I
44	426.5	76.0	124	2 S40336	Ig kappa chain V-J
45	426	75.9	108	1 K1H0U1	Ig kappa chain V-I

ALIGNMENTS

```
RESULT 1
S52447
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52447
R:Berdoz, J.; Kraehenbuhl, J.P.
Submitted to the EMBL Data Library, November 1994
A:Description: Specific amplification by the polymerase chain reaction of rearranged ge
A:Reference number: S52445
A:Accession: S52447
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-127 <BER>
A:Cross-references: EMBL:X82688; NID:G673443; PIDN:CAA58009.1; PID:G673444
C:Genetics:
A:Insertions: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMW>

Query Match      86.6%; Score 486; DB 2; Length 127;
Best Local Similarity 83.2%; Pred. No. 7.1e-35;
Matches 89; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY      1 DIQWTQSPSSLSASVGDRTVITCKASQDISYSWFQOKPKAKPTLIYRANLVDCVPS 60
      ||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      21 DIQWTQSPSSMVASLGERVITITCKASQDINNVIAMWQOKGKSPKTLIYRANLVDCVPS 80
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      61 RFSGSGSGQDYTTTISLQPEDPATYTCLOYDEPFYFGGKTVK 107
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      81 RFSGSGSGQDYTTTISLQPEDPATYTCLOYDEPFYFGGKTVK 127
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 2
KVMST1
Ig kappa chain precursor V region (TI) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1980 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
C:Accession: A01920
R:Altendurger, W.; Steimetz, M.; Zachau, H.G.
Nature 287, 603-607, 1980
A:Title: Functional and non-functional joining in immunoglobulin light chain genes of a
A:Reference number: A01920; MUID:81052342; PMID:6776411
A:Accession: A01920
A:Molecule type: mRNA
A:Residues: 1-128 <ALT>
A:Cross-references: UNIPROT:P01637; GB:V00772; NID:G51636; PIDN:CAA24150.1; PID:G762979
A>Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Insertions: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
```

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1d
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer
 F/1-20/Domain: signal sequence #status predicted <SIG>
 F/21-128/Product: Ig kappa chain V region (TL) #status predicted <MAT>
 F/36-110/Domain: immunoglobulin homology <IMM>
 F/43-108/Disulfide bonds: #status predicted

Query Match 84.5%; Score 474; DB 1; Length 128;
 Best Local Similarity 81.3%; Pred. No. 7.6e-34;
 Matches 87; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSMFQOKPGKAPKTLIYRANRLVDGVP 60
 DB 21 DIKMTQSPSSMYASIGERVITCKASQDINSYLSMFQOKPGKSPKTLIYRANRLVDGVP 80
 QY 61 RFGSGSGODYTLTSSIQPEDPATYTCLOYDEFPYFGGTKEIK 107
 DB 81 RFGSGSGODYTLTSSILEYDMGIYCYLODEFPFLFGAGTKLEIK 127

RESULT 3

Ig kappa chain precursor (15C5) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C/Accession: S14237
 R/Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
 Eur. J. Biochem. 192, 767-775, 1990
 A/Title: Construction and characterization of a recombinant murine monoclonal antibody
 A/Reference number: S14236; MUID:91006173; PMID:2209622
 A/Accession: S14237
 A/Molecule type: mRNA
 A/Residues: 1-234 <YAN>
 A/Cross-references: EMBL:X56394; NID:951622; PIDN:CA939805.1; PID:951623
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 470; DB 2; Length 234;
 Best Local Similarity 81.3%; Pred. No. 3e-33;
 Matches 87; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSMFQOKPGKAPKTLIYRANRLVDGVP 60
 DB 21 DIKMTQSPSSMYASIGERVITCKASQDINSYLSMFQOKPGKSPKTLIYRANRLVDGVP 80
 QY 61 RFGSGSGODYTLTSSIQPEDPATYTCLOYDEFPYFGGTKEIK 107
 DB 81 RFGSGSGODYTLTSSILEYDMGIYCYLODEFPFLFGAGTKLEIK 127

RESULT 4

Ig kappa chain precursor V region (40-140) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
 C/Accession: P10101
 R/Near, R.I.; Haber, E.
 Mol. Immunol. 26, 371-382, 1989
 A/Title: Characterization of the heavy and light chain immunoglobulin variable region
 A/Reference number: P10100; MUID:89238344; PMID:2497340
 A/Accession: P10101
 A/Molecule type: DNA
 A/Residues: 1-128 <NEA>
 A/Experimental source: strain A/J
 A/Note: the V40-140 gene segment can be classified as a member of the V49 subgroup
 C/Genetics:
 A/Insertions: 17/1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/1-20/Domain: signal sequence #status predicted <SIG>
 F/21-114/Domain: V segment #status predicted <VRS>

F/36-110/Domain: immunoglobulin homology <IMM>
 F/115-128/Domain: J segment #status predicted <JNE>

Query Match 81.8%; Score 459; DB 2; Length 128;
 Best Local Similarity 80.4%; Pred. No. 1.5e-32;
 Matches 86; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSMFQOKPGKAPKTLIYRANRLVDGVP 60
 DB 21 DIKMTQSPSSMYASIGERVITCKASQDINSYLSMFQOKPGKSPKTLIYRANRLVDGVP 80
 QY 61 RFGSGSGODYTLTSSIQPEDPATYTCLOYDEFPYFGGTKEIK 107
 DB 81 RFGSGSGODYTLTSSILEYDMGIYCYLODEFPFLFGAGTKLEIK 127

RESULT 5

Ig kappa chain V region - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C/Accession: S52789
 R/Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoy, L.; Deret,
 submitted to the EMBL Data Library, March 1995
 A/Description: Light chain V region gene usage restriction and peculiarities in myeloma-
 A/Reference number: S52789
 A/Accession: S52789
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-129 <ROC>
 A/Cross-references: EMBL:X85995; NID:9758588; PIDN:CA95987.1; PID:9758589
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/38-112/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 453; DB 2; Length 129;
 Best Local Similarity 80.4%; Pred. No. 4.8e-32;
 Matches 86; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSMFQOKPGKAPKTLIYRANRLVDGVP 60
 DB 23 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSMFQOKPGKAPKTLIYRANRLVDGVP 82
 QY 61 RFGSGSGODYTLTSSIQPEDPATYTCLOYDEFPYFGGTKEIK 107
 DB 83 RFGSGSGODYTLTSSILEYDMGIYCYLODEFPFLFGAGTKLEIK 129

RESULT 6

Ig kappa chain V-J region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S40333
 R/Klein, R.; Uenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin ch1 genes and their hypermutation.
 A/Reference number: S40332; MUID:94080891; PMID:8258341
 A/Accession: S40333
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-125 <KLE>
 A/Cross-references: EMBL:X72443; NID:9441354; PIDN:CA51111.1; PID:9441355
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 452; DB 2; Length 125;
 Best Local Similarity 78.5%; Pred. No. 5.7e-32;
 Matches 84; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSMFQOKPGKAPKTLIYRANRLVDGVP 60
 DB 21 DIKMTQSPSSMYASIGERVITCKASQDINSYLSMFQOKPGKSPKTLIYRANRLVDGVP 80
 QY 61 RFGSGSGODYTLTSSIQPEDPATYTCLOYDEFPYFGGTKEIK 107
 DB 81 RFGSGSGODYTLTSSILEYDMGIYCYLODEFPFLFGAGTKLEIK 127

Db 19 DIQWTOGSPSSLSASVGDRTVITTCRASQSSISMLAWYQOKPGKAKKLIIYANRLVDSVPS 78
QY 61 RFSSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTKEIK 107
Db 79 RFSSGSGGTFTLTISLQPEDPATYTCQOYNSYPTTFGGGTKEIK 125

RESULT 7

36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C/Accession: S36264
R/Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993.
A/Title: Human anti-self antibodies with high specificity from phage display libraries.
A/Reference number: S36264; MUID:93178448; PMID:7679990
A/Accession: S36264
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-107 <GRL>
A/Cross-references: EMBL:Z18845; NID:933426; PIRN:CAA79297.1; PID:9339919
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 451; DB 2; Length 107;
Best Local Similarity 79.4%; Pred. No. 6e-32;

Matches 85; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTOGSPSSLSASVGDRTVITTCRASQDINSYLSWFOQKPKAKKLIIYANRLVDSVPS 60
Db 1 EIVLTQSPSSLSASVGDRTVITTCRASQSSISYLMWYQOKPGKAKKLIIYANRLVDSVPS 60
QY 61 RFSSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTKEIK 107
Db 61 RFSSGSGGTFTLTISLQPEDPATYTCQOYNSYPTTFGGGTKEIK 107

RESULT 8

849047
Ig kappa chain V region (monoclonal strictional autoantibody Strab SA-1A) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B49047
R/Victor, K.D.; Fasnau, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A/Title: Human monoclonal strictional autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID:92387224; PMID:1516616
A/Accession: B49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-108 <VIC>
A/Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A/Experimental source: thymic B lymphocytes
C/Note: sequence extracted from NCBI backbone (NCBI:113208, NCBI:113209)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 451; DB 2; Length 108;
Best Local Similarity 82.2%; Pred. No. 6e-32;

Matches 88; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQWTOGSPSSLSASVGDRTVITTCRASQDINSYLSWFOQKPKAKKLIIYANRLVDSVPS 60
Db 1 DIQWTOGSPSSLSASVGDRTVITTCRASQSSISYLMWYQOKPGKAKKLIIYANRLVDSVPS 60
QY 61 RFSSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTKEIK 107
Db 61 RFSSGSGGTFTLTISLQPEDPATYTCQOYNSYPTTFGGGTKEIK 107

RESULT 9

540334
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40334
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40334; MUID:94080891; PMID:8258341
A/Accession: S40334
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-132 <KLB>
A/Cross-references: EMBL:X72444
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/37-111/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 450; DB 2; Length 132;
Best Local Similarity 77.6%; Pred. No. 8.8e-32;

Matches 83; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQWTOGSPSSLSASVGDRTVITTCRASQDINSYLSWFOQKPKAKKLIIYANRLVDSVPS 60
Db 22 DIQWTOGSPSSLSASVGDRTVITTCRASQSSISYLMWYQOKPGKAKKLIIYANRLVDSVPS 81
QY 61 RFSSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTKEIK 107
Db 82 RFSSGSGGTFTLTISLQPEDPATYTCQOYNSYPTTFGGGTKEIK 128

RESULT 10

540369
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40369
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40369; MUID:94080891; PMID:8258341
A/Accession: S40369
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-129 <KLB>
A/Cross-references: EMBL:X72479; NID:9441426; PIRN:CAA51147.1; PID:9441427
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/37-111/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 449; DB 2; Length 129;
Best Local Similarity 79.4%; Pred. No. 1.1e-31;

Matches 85; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQWTOGSPSSLSASVGDRTVITTCRASQDINSYLSWFOQKPKAKKLIIYANRLVDSVPS 60
Db 22 DIQWTOGSPSSLSASVGDRTVITTCRASQSSISYLMWYQOKPGKAKKLIIYANRLVDSVPS 81
QY 61 RFSSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTKEIK 107
Db 82 RFSSGSGGTFTLTISLQPEDPATYTCQOYNSYPTTFGGGTKEIK 128

RESULT 11

540313
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40313
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40313; MUID:94080891; PMID:8258341

A/Accession: S40313
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-123 <RES>
 A/Cross-references: EMBL:X72423; NID:G441314; PIDN:CAA51091.1; PID:G441315
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/32-106/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 447; DB 2; Length 123;
 Best Local Similarity 81.3%; Pred. No. 1.5e-31;
 Matches 87; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAPKTLTYRANRLVDGVPS 60
 DB 17 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAPKTLTYRANRLVDGVPS 76
 QY 61 RFGSGSGQDYTLTISLQPEDPATYTCLODYDEFPYTFGGGTKEIK 107
 DB 77 RFGSGSGGTEFTLTISLQPEDPATYTCLODYDEFPYTFGGGTKEIK 123

RESULT 12

IG kappa chain V region - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C/Accession: S20652
 R/Losman, M.; Pasy, T.M.; Novick, K.E.; Monestier, M.
 Submitted to the EMBL Data Library, February 1992
 A/Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
 A/Reference number: S20639
 A/Accession: S20652
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-106 <LOS>
 A/Cross-references: EMBL:X65008; NID:G52649; PINN:CAA6141.1; PID:G52650
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 446; DB 2; Length 106;
 Best Local Similarity 77.4%; Pred. No. 1.6e-31;
 Matches 82; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAPKTLTYRANRLVDGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAPKTLTYRANRLVDGVPS 60
 QY 61 RFGSGSGQDYTLTISLQPEDPATYTCLODYDEFPYTFGGGTKEIK 106
 DB 61 RFGSGSGGLYFSLISLSEYEDMGICYCQYDDFPYTFGGGTKEIK 106

RESULT 13

IG kappa chain V-I region (Au) - human
 C/Species: Homo sapiens (man)
 C/Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
 C/Accession: A91633; A01862; S02573
 R/Schleich, H.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
 A/Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette vom kappa-Typ, Sub
 A/Reference number: A91653; MUID:72189444; PMID:5028201
 A/Accession: A91653
 A/Molecule type: Protein
 A/Residues: 1-108 <SCH>
 A/Cross-references: UNIPROT:P01594
 A/Note: the C region of this chain has the Inv (3) marker
 R/Fehlhammer, H.; Schiffer, M.; Bpp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei
 Biophys. Struct. Mech. 1, 139-146, 1975
 A/Title: The structure determination of the variable portion of the Bence-Jones protein
 A/Reference number: A90729; MUID:77022433; PMID:1234024

A/Contents: annotation; X-ray crystallography
 A/Note: the structure of the V region was determined by molecular replacement methods
 R/Steiner, V.; Chang, J.Y.
 FEBS Lett. 222, 6-10, 1987
 A/Title: Chemical modification of the carboxyl groups of protein substrates enhances ti
 A/Reference number: S02572; MUID:88005152; PMID:3115831
 A/Contents: annotation
 C/Comment: This is a Bence Jones protein.
 C/Genetics:
 A/Gene: GDB:IGKV1
 A/Cross-references: GDB:136264
 A/Map position: 2p12-2p12

A/Complex: an immunoglobulin heterotetramer subunit consists of two identical light (ka
 chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>
 F/23-86/Disulfide bonds: #status predicted

Query Match 79.1%; Score 444; DB 1; Length 108;
 Best Local Similarity 79.4%; Pred. No. 2.4e-31;
 Matches 85; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAPKTLTYRANRLVDGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAPKTLTYRANRLVDGVPS 60
 QY 61 RFGSGSGQDYTLTISLQPEDPATYTCLODYDEFPYTFGGGTKEIK 107
 DB 61 RFGSGSGAHFTFTLTISLQPEDPATYTCLODYDEFPYTFGGGTKEIK 107

RESULT 14

IG kappa chain (BRB) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
 C/Accession: I39154
 R/Schormann, N.; Murrell, J.R.; Liepnieske, J.J.; Benson, M.D.
 Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
 A/Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A propose
 A/Reference number: I39154; MUID:96003804; PMID:7568160
 A/Accession: I39154
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-108 <RES>
 A/Cross-references: EMBL:U3144; NID:G944925; PIDN:AAV79238.1; PID:G944926
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 444; DB 2; Length 108;
 Best Local Similarity 80.4%; Pred. No. 2.4e-31;
 Matches 86; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAPKTLTYRANRLVDGVPS 60
 DB 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKAPKTLTYRANRLVDGVPS 60
 QY 61 RFGSGSGQDYTLTISLQPEDPATYTCLODYDEFPYTFGGGTKEIK 107
 DB 61 RFGSGSGTEFTLTISLQPEDPATYTCLODYDEFPYTFGGGTKEIK 107

RESULT 15

IG kappa chain V-J region - human
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C/Accession: S40349
 R/Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A/Title: Expressed human immunoglobulin chl genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341
 A;Accession: S40349
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-125 <KLE>
 A;Cross-references: EMBL:X72459; NID:9441386; PIDN:CAA51127.1; PID:9441387
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 444; DB 2; length 125;
 Best local similarity 80.2%; Pred. No. 2.7e-31;
 Matches 85; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 2 IQMTQSPSSISASVGDVITTCASQDINSYLSWFOQPGKAPKTLITYRANRLVDGVPSSR 61
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 19 IQLTQSPSSISASVGDVITTCRASQGISALAWYQOKPGCAPKTLITYDASSLSGVPSSR 78
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Qy 62 FSGSGSGQDYTLTISLQPEDFATYCYCLOYDEPPYTFGGGTKEIK 107
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 79 FSGSGSGCTDFTLTISLQPEDFATYCCQGFNTYPLTFGGGTKEIK 124
 ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: December 29, 2004, 18:06:58
 Job time : 14.8437 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW protein - protein search, using SW model

Run on: December 29, 2004, 18:05:34 ; Search time 61.8643 Seconds
(without alignments)
622.182 Million cell updates/sec

Title: US-10-774-076-14

Perfect score: 561
Sequence: 1 DIQMTQSPSSLSASVDGRVT.....CLQYDEPFYFGGCTKVEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications AA:
2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	561	100.0	107	US-10-774-076-14	Sequence 14, App1
2	561	100.0	127	US-10-774-076-19	Sequence 19, App1
3	510	90.9	107	US-09-158-120A-20	Sequence 20, App1
4	503	89.7	107	US-10-774-076-3	Sequence 3, App1
5	503	89.7	127	US-10-774-076-11	Sequence 11, App1
6	502	89.5	107	US-10-340-189-27	Sequence 27, App1
7	502	89.5	107	US-10-325-966-27	Sequence 27, App1
8	499	88.9	107	US-10-462-062-107	Sequence 107, App
9	499	88.9	107	US-10-472-905A-96	Sequence 96, App1
10	499	88.9	127	US-10-462-062-182	Sequence 182, App
11	499	88.9	127	US-10-472-905A-122	Sequence 122, App
12	498	88.8	107	US-10-127-890-125	Sequence 125, App
13	498	88.8	107	US-10-340-189-87	Sequence 87, App1

14	498	88.8	107	US-10-325-696-65	Sequence 65, App1
15	496	88.4	107	US-10-436-782-33	Sequence 33, App1
16	496	88.4	107	US-10-436-783-1	Sequence 1, App1
17	495	88.2	240	US-10-127-890-147	Sequence 147, App
18	495	88.2	240	US-10-127-890-148	Sequence 148, App
19	493	87.9	107	US-10-462-062-99	Sequence 99, App1
20	493	87.9	107	US-10-472-905A-88	Sequence 88, App1
21	493	87.9	127	US-10-462-062-180	Sequence 180, App
22	493	87.9	127	US-10-472-905A-120	Sequence 120, App
23	491	87.5	107	US-10-412-406-8	Sequence 8, App1
24	491	87.5	663	US-10-412-406-32	Sequence 32, App1
25	491	87.5	4852	US-10-412-406-33	Sequence 33, App1
26	489	87.2	107	US-10-462-062-93	Sequence 93, App1
27	489	87.2	107	US-10-472-905A-82	Sequence 82, App1
28	489	87.2	127	US-10-462-062-179	Sequence 179, App
29	489	87.2	127	US-10-472-905A-119	Sequence 119, App
30	487	86.8	107	US-10-462-062-101	Sequence 101, App
31	487	86.8	107	US-10-462-062-109	Sequence 109, App
32	487	86.8	107	US-10-472-905A-90	Sequence 90, App1
33	487	86.8	107	US-10-472-905A-98	Sequence 98, App1
34	487	86.8	127	US-10-462-062-181	Sequence 181, App
35	487	86.8	127	US-10-462-062-183	Sequence 183, App
36	487	86.8	127	US-10-472-905A-121	Sequence 121, App
37	487	86.8	127	US-10-472-905A-123	Sequence 123, App
38	485	86.5	107	US-10-412-406-4	Sequence 4, App1
39	483	85.1	107	US-10-412-406-6	Sequence 6, App1
40	482	85.9	107	US-10-340-189-26	Sequence 26, App1
41	482	85.9	107	US-10-325-696-26	Sequence 26, App1
42	473	84.3	142	US-09-797-481-2	Sequence 2, App1
43	473	84.3	142	US-09-844-736-4	Sequence 4, App1
44	473	84.3	142	US-10-162-396-4	Sequence 4, App1
45	473	84.3	142	US-10-819-493-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-10-774-076-14
; Sequence 14, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Antipeptide Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-774-076-14

Query Match 100.0%; Score 561; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVDGRVTITCKASQDINSYLSWFOQKRGKAPKTLIYRANLVGVPS 60
Db 1 DIQMTQSPSSLSASVDGRVTITCKASQDINSYLSWFOQKRGKAPKTLIYRANLVGVPS 60
QY 61 REGSGSGQDYTLTISSLPEDPATYTCLOYPDEFYFGGCTKVEIK 107
Db 61 REGSGSGQDYTLTISSLPEDPATYTCLOYPDEFYFGGCTKVEIK 107
RESULT 2

US-10-774-076-19
; Sequence 19, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-774-076-19

Query Match 100.0%; Score 561; DB 17; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGRVTTTCASODINSYLSWFOQKPKAPKTLIYRANRLVDGVPS 60
DB 21 DIQMTSPSSLSASVGRVTTTCASODINSYLSWFOQKPKAPKTLIYRANRLVDGVPS 80
QY 61 RFSGSGSGDYTLTISLSLOPEDPATYCYCLOYDEFPYTFGGGTKEIK 107
DB 81 RFSGSGSGDYTLTISLSLOPEDPATYCYCLOYDEFPYTFGGGTKEIK 127

RESULT 3
US-09-158-120A-20
; Sequence 20, Application US/09158120A
; Patent No. US20020102257A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, L.
; TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIV, GILFILLAN, CECCHI,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: P160
; OPERATING SYSTEM: Windows95
; SOFTWARE: MS Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/158,120A
; FILING DATE: September 21, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,592
; FILING DATE: August 15, 1994
; APPLICATION NUMBER: 07/813,372
; FILING DATE: December 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 469201-367
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
; LENGTH: 107 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-158-120A-20

Query Match 90.9%; Score 510; DB 9; Length 107;
Best Local Similarity 88.8%; Pred. No. 3.7e-36;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGRVTTTCASODINSYLSWFOQKPKAPKTLIYRANRLVDGVPS 60
DB 1 DIQMTSPSSLSASVGRVTTTCASODINSYLSWFOQKPKAPKTLIYRANRLVDGVPS 60
QY 61 RFSGSGSGDYTLTISLSLOPEDPATYCYCLOYDEFPYTFGGGTKEIK 107
DB 61 RFSGSGSGDYTLTISLSLOPEDPATYCYCLOYDEFPYTFGGGTKEIK 107

RESULT 4
US-10-774-076-3
; Sequence 3, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-3

Query Match 89.7%; Score 503; DB 17; Length 107;
Best Local Similarity 87.9%; Pred. No. 1.4e-35;
Matches 94; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGRVTTTCASODINSYLSWFOQKPKAPKTLIYRANRLVDGVPS 60
DB 1 DIQMTSPSSLSASVGRVTTTCASODINSYLSWFOQKPKAPKTLIYRANRLVDGVPS 60
QY 61 RFSGSGSGDYTLTISLSLOPEDPATYCYCLOYDEFPYTFGGGTKEIK 107
DB 61 RFSGSGSGDYTLTISLSLOPEDPATYCYCLOYDEFPYTFGGGTKEIK 107

RESULT 5
US-10-774-076-11
; Sequence 11, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 127
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-11

;; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;; FILE REFERENCE: 053466-0360
;; CURRENT APPLICATION NUMBER: US/10/462,062
;; CURRENT FILING DATE: 2003-06-16
;; PRIOR APPLICATION NUMBER: PCT/JP99/01768
;; PRIOR FILING DATE: 1999-04-02
;; PRIOR APPLICATION NUMBER: JP 10-91850
;; PRIOR FILING DATE: 1998-04-03
;; NUMBER OF SEQ ID NOS: 183
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 107
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
;; OTHER INFORMATION: for version "b1" of humanized L chain V region
US-10-462-062-107

Query Match 88.9%; Score 499; DB 15; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.2e-35;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRKASODINSLYLSWFOQKPKGAPKTLIYRANRLVDGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRKASODIKSFLSWFOQKPKGSKPTLIYATSLADGVPS 60
QY 61 RFSGSGSGQDYTLTISLQPEDFATYYCLOYDEFPYTFGGGTKEIK 107
Db 61 RFSGSGSGDYTLTISLQPEDFATYYCLOYDEFPYTFGGGTKEIK 107

RESULT 9
US-10-472-905A-96

;; Sequence 96, Application US/10472905A
;; Publication No. US20040180051A1
;; GENERAL INFORMATION:
;; APPLICANT: SUZUKI, KOJI
;; TITLE OF INVENTION: BLOOD RHEOLOGY-IMPROVING AGENT
;; FILE REFERENCE: 053466-0368
;; CURRENT APPLICATION NUMBER: US/10/472,905A
;; CURRENT FILING DATE: 2003-09-25
;; PRIOR APPLICATION NUMBER: PCT/JP02/02933
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: JP 2001-088387
;; PRIOR FILING DATE: 2001-03-26
;; NUMBER OF SEQ ID NOS: 123
;; SOFTWARE: Patentin Ver. 3.2
;; SEQ ID NO 96
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: amino acid sequence of version "b1" of humanized L
;; OTHER INFORMATION: chain V region
US-10-472-905A-96

Query Match 88.9%; Score 499; DB 16; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.2e-35;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRKASODINSLYLSWFOQKPKGAPKTLIYRANRLVDGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITTCRKASODIKSFLSWFOQKPKGSKPTLIYATSLADGVPS 60
QY 61 RFSGSGSGQDYTLTISLQPEDFATYYCLOYDEFPYTFGGGTKEIK 107
Db 61 RFSGSGSGDYTLTISLQPEDFATYYCLOYDEFPYTFGGGTKEIK 107

RESULT 10
US-10-462-062-182

;; Sequence 182, Application US/10462062
;; Publication No. US20040044187A1
;; GENERAL INFORMATION:
;; APPLICANT: SATO, KOH
;; APPLICANT: ADACHI, HIDEKI
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
;; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;; FILE REFERENCE: 053466-0360
;; CURRENT APPLICATION NUMBER: US/10/462,062
;; CURRENT FILING DATE: 2003-06-16
;; PRIOR APPLICATION NUMBER: PCT/JP99/01768
;; PRIOR FILING DATE: 1999-04-02
;; PRIOR APPLICATION NUMBER: JP 10-91850
;; PRIOR FILING DATE: 1998-04-03
;; NUMBER OF SEQ ID NOS: 183
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 182
;; LENGTH: 127
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
;; OTHER INFORMATION: sequence of version "b1" of humanized L chain V region
US-10-462-062-182

Query Match 88.9%; Score 499; DB 15; Length 127;
Best Local Similarity 89.7%; Pred. No. 3.8e-35;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRKASODINSLYLSWFOQKPKGAPKTLIYRANRLVDGVPS 60
Db 21 DIQMTQSPSSLSASVGRVITTCRKASODIKSFLSWFOQKPKGSKPTLIYATSLADGVPS 80
QY 61 RFSGSGSGQDYTLTISLQPEDFATYYCLOYDEFPYTFGGGTKEIK 107
Db 81 RFSGSGSGDYTLTISLQPEDFATYYCLOYDEFPYTFGGGTKEIK 127

RESULT 11

US-10-472-905A-122
;; Sequence 122, Application US/10472905A
;; Publication No. US20040180051A1
;; GENERAL INFORMATION:
;; APPLICANT: SUZUKI, KOJI
;; TITLE OF INVENTION: BLOOD RHEOLOGY-IMPROVING AGENT
;; FILE REFERENCE: 053466-0368
;; CURRENT APPLICATION NUMBER: US/10/472,905A
;; CURRENT FILING DATE: 2003-09-25
;; PRIOR APPLICATION NUMBER: PCT/JP02/02933
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: JP 2001-088387
;; PRIOR FILING DATE: 2001-03-26
;; NUMBER OF SEQ ID NOS: 123
;; SOFTWARE: Patentin Ver. 3.2
;; SEQ ID NO 122
;; LENGTH: 127
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: amino acid sequence of version "b1" of
;; OTHER INFORMATION: humanized L chain V region
US-10-472-905A-122

Query Match 88.9%; Score 499; DB 16; Length 127;
Best Local Similarity 89.7%; Pred. No. 3.8e-35;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRKASODINSLYLSWFOQKPKGAPKTLIYRANRLVDGVPS 60
Db 21 DIQMTQSPSSLSASVGRVITTCRKASODIKSFLSWFOQKPKGSKPTLIYATSLADGVPS 80
QY 61 RFSGSGSGQDYTLTISLQPEDFATYYCLOYDEFPYTFGGGTKEIK 107

Db 81 RFGSGSGTDYTLTISLQPEDFATYTCLOHGESPTFGGTVEIK 127

RESULT 12
US-10-127-990-125
; Sequence 125, Application US/10127890
; Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-May-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-May-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-May-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-Dec-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-Jun-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-Nov-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-10-127-990-125
Query Match 88.8%; Score 498; DB 14; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.9e-35;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVDGVITTCASQDINSYLSWFOQKRGKAPKTLIYRANRLVDGVP 60
Db 1 DIQMTQSPSSLSASVDGVITTCASQDINSYLSWFOQKRGKAPKTLIYRANRLVDGVP 60
QY 61 RFGSGSGGODYTLTISLQPEDFATYTCLOHGESPTFGGTVEIK 107
Db 61 RFGSGSGGTDYTLTISLQPEDFATYTCLOHGESPTFGGTVEIK 107

RESULT 13
US-10-340-189-87
; Sequence 87, Application US/10340189
; Publication No. US20030229207A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 W. Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-Jun-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-Dec-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-Dec-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-10-340-189-87
Query Match 88.8%; Score 498; DB 14; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.9e-35;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVDGVITTCASQDINSYLSWFOQKRGKAPKTLIYRANRLVDGVP 60
Db 1 DIQMTQSPSSLSASVDGVITTCASQDINSYLSWFOQKRGKAPKTLIYRANRLVDGVP 60
QY 61 RFGSGSGGODYTLTISLQPEDFATYTCLOHGESPTFGGTVEIK 107
Db 61 RFGSGSGGTDYTLTISLQPEDFATYTCLOHGESPTFGGTVEIK 107
RESULT 14
US-10-325-696-65
; Sequence 65, Application US/10325696
; Publication No. US20040005630A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 67

```

CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US06/200-71.PL.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9050
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-325-696-65

Query Match      88.8%; Score 498; DB 15; Length 107;
Best Local Similarity 89.7%; Pred. No. 3.9e-35;
Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIGNTPSSLSASVGDRTVTTCASQDINSYLSWFOQKPKAKPTLIYRANRLVDGVP 60
DB 1 DIGNTPSSLSASVGDRTVTTCASQDINSYLSWFOQKPKAKPTLIYRANRLVDGVP 60
QY 61 RFGSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTYEIK 107
DB 61 RFGSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTYEIK 107

RESULT 15
US-10-436-782-33
Sequence 33: Application US/10436782
Publication No. US2004028685A1
GENERAL INFORMATION:
APPLICANT: Kinch, Michael
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Kiener, Peter
APPLICANT: Langermann, Solomon
TITLE OF INVENTION: EphA2 Monoclonal Antibodies and Methods of Use Thereof
FILE REFERENCE: 10271-097
CURRENT APPLICATION NUMBER: US/10/436,782
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,322
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2002-10-14
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2003-04-03

```

```

; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-436-782-33

Query Match      88.4%; Score 496; DB 15; Length 107;
Best Local Similarity 86.0%; Pred. No. 5.7e-35;
Matches 92; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIGNTPSSLSASVGDRTVTTCASQDINSYLSWFOQKPKAKPTLIYRANRLVDGVP 60
DB 1 DIGNTPSSLSASVGDRTVTTCASQDINSYLSWFOQKPKAKPTLIYRANRLVDGVP 60
QY 61 RFGSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTYEIK 107
DB 61 RFGSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTYEIK 107

Search completed: December 29, 2004, 18:42:01
Job time : 62.8643 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:37:57 ; Search time 73.5428 Seconds
(without alignments)
521.928 Million cell updates/sec

Title: US-10-774-076-14

Perfect score: 561
Sequence: 1 DQMTQSPSSLSASVDGRVT.....CLQYDERPPTFGGKTKVEIK 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_GeneSeq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520	92.7	107	2	AAW23953
2	520	92.7	240	2	AAW23954
3	514	91.6	107	6	ABG74710
4	514	91.6	107	7	ABR83157
5	514	91.6	214	6	ABG74711
6	514	91.6	214	7	ABR83150
7	510	90.9	107	2	AAW23953
8	510	90.9	107	5	ABG31429
9	510	90.9	129	2	AAW23954
10	510	90.9	129	2	AAW23954
11	510	90.9	129	5	ABG31444
12	502	89.5	107	2	AAW23953
13	502	89.5	107	8	AD101168
14	499	88.9	107	2	AAW23953
15	499	88.9	107	6	ABG74710
16	499	88.9	107	6	ABG74710
17	498	88.8	107	2	AAW23953
18	498	88.8	107	2	AAW23953
19	496	88.4	107	8	AD101168
20	496	88.4	107	8	AD101168
21	496	88.4	107	8	AD101168
22	494	88.1	237	7	AD101168
23	494	88.1	237	7	AD101168
24	494	88.1	237	7	AD101168
25	494	88.1	246	4	AAW23953

26	493	87.9	107	2	AAW23953	AAW23953	Humanised
27	493	87.9	107	6	ABG74710	ABG74710	Humanised
28	493	87.9	107	6	ABG74710	ABG74710	Humanised
29	491	87.5	107	5	ABR83157	ABR83157	Humanised
30	491	87.5	214	2	AAW23953	AAW23953	Humanised
31	491	87.5	214	5	ABG31429	ABG31429	Humanised
32	491	87.5	355	2	AAW23953	AAW23953	Humanised
33	491	87.5	355	2	AAW23953	AAW23953	Humanised
34	491	87.5	358	2	AAW23953	AAW23953	Humanised
35	491	87.5	358	2	AAW23953	AAW23953	Humanised
36	491	87.5	360	2	AAW23953	AAW23953	Humanised
37	491	87.5	379	2	AAW23953	AAW23953	Humanised
38	489	87.2	107	2	AAW23953	AAW23953	Humanised
39	489	87.2	107	4	AAW23953	AAW23953	Humanised
40	489	87.2	107	6	ABG74710	ABG74710	Humanised
41	489	87.2	127	6	ABG74710	ABG74710	Humanised
42	487	86.8	107	2	AAW23953	AAW23953	Humanised
43	487	86.8	107	2	AAW23953	AAW23953	Humanised
44	487	86.8	107	4	AAW23953	AAW23953	Humanised
45	487	86.8	107	4	AAW23953	AAW23953	Humanised

ALIGNMENTS

RESULT 1	AAW23953	standard; protein; 107 AA.
ID	AAW23953	
AC	AAW23953	
XX		
DT	17-OCT-2003	(revised)
DT	17-JUN-1998	(first entry)
XX		
DE	Chimeric humanised Mus musculus A717 antibody heavy chain.	
XX		
KW	Chimeric; humanised; human; murine; A717; antibody; heavy chain;	
KW	variable region; diabetes; prophylactic treatment.	
XX		
OS	Mus musculus.	
OS	Homo sapiens.	
OS	Chimeric.	
XX		
PN	NO9749429-A1.	
XX		
PD	31-DEC-1997.	
XX		
PF	26-JUN-1997;	97MO-US011605.
XX		
PR	27-JUN-1996;	96US-00672176.
XX		
PA	(EXOC-) EXOCCEL INC.	
XX		
PI	Cohen MP, Shearman CW;	
XX		
DR	WPI, 1998-076916/07.	
XX		
PT	N-PSDB; AA04637.	
PT	New humanised antibodies specific for glycated albumin - prepared by	
PT	recombinant expression of humanised mouse antibodies, useful for, e.g.	
PT	treating diabetic vasculopathy.	
XX		
XX		
PS	Example 2; Page 15; 27p; English.	
XX		
CC	The sequence is that of a humanised variable region of the A717 antibody	
CC	light chain VL-1. The antibody has specificity for glycated albumin (GA)	
CC	and is capable of neutralising the effects of GA in vivo. It can be used	
CC	in the manufacture of therapeutics useful for the prophylactic treatment	
CC	of complications of diabetes (especially diabetic vasculopathy and	
CC	retinopathy) and atherosclerotic cardiovascular disease. The genetically	
CC	engineered antibodies are specific as they only interact with GA but not	
CC	other proteins and may be easily prepared in pure form. (Updated on 17-	
CC	OCT-2003 to standardise OS field)	

XX Sequence 107 AA;
SQ

Query Match	92.7%	Score 520;	DB 2;	Length 107;
Best Local Similarity	92.5%	Pred. No. 8.5e-33;		
Matches 99;	Conservative 4;	Mismatches 4;		Indels

Qy	1D1OMTOSBSLSASIGEDRVTTTTCASODINSYLSWFOOKGKAPKTLIYRANRLVNGVPS	60
Db	1D1OMTOSBSLSASIGEDRVTTTTCASODINSYLSWFOOKGKAPKSLIYHTRRLDGVPS	60
Qy	61RSSGGSGQDYTLTITSSLOPEDFATYVCLQYDEEPPYFGGSGTVEIK	107
Db	61RSSGGSGQDYTLTITSSLOPEDFATYVCLQYDEEPPYFGGSGTVEIK	107

RESULT 2	
AAW23954	
ID	AAW23954
XX	standard; protein; 240 AA.

XX	
XX	
XX	
AC	AAM23954;
17-OCT-2003	(revised)
17-JUN-1998	(first entry)
XX	
DE	Chimeric humanised Mus musculus A717 antibody ScFv.
XX	

XX	Mus musculus.
KW	Homo sapiens.
DS	Chimeric.

27-JUN-1996;	96US-00672176
26-JUN-1997;	97WO-US011605
31-DEC-1997.	
WO9749429-A1.	

(EXOC-) EXOCCELL INC.
Cohen MP, Shearman CW;
WPI, 1998-076916/07.
N-PSDB; AAV04638.

New humanised antibodies specific for glycated albumin - prepared by recombinant expression of humanised mouse antibodies, useful for, e.g. treating diabetic vasculopathy.

Example 3; Page 15-16; 27pp; English.

The sequence is that of a humanised variable region of the A717 antibody ScFv, huA17-ScFv. The antibody has specificity for glycated albumin (GA) and is capable of neutralising the effects of GA *in vivo*. It can be used in the manufacture of therapeutics useful for the prophylactic treatment of complications of diabetes (especially diabetic vasculopathy and retinopathy) and atherosclerotic cardiovascular disease. The genetically engineered antibodies are specific as they only interact with GA but not other proteins and may be easily prepared in pure form. (Updated on 17-Oct-2003 to standardise OS field)

Sequence 240 AA;

Query Match	92.7%;	Score 520;	DB 2;	Length 240;
Best Local Similarity	92.5%;	Pred. No. 1.8e-32;		
Matches	99;	Conservative	4;	Mismatches 4;

1 DIOMTQSPSSLSASVGVDRVTITCKASODINSYLSWFOQKPGKAPKLLIYRANRLVDGVPS 60

Db 134 DIGNTPSSLSAVGDRVTITCKASQDIDSYLSMFPQCKPKAPKSLIYHNRLLDGVPS 193

```

Wy      61  RFGSGSGGQDYTLTISLQPEDPATYCYCQYDEFPYTFGGGKVEIK 107
        | | | | | : | | | | | | | | | | | | | | | | | |
Db      194  RFGSGSGGTDFTLTISLQPEDPATYCYCQYDEFPPTFGGKVEIK 240

```

```

RESULT 3
ABG74710
ID      ABG74710 standard; protein; 107 AA
XX

```

AC	ABG/4710;	
XX		
DT	10-MAY-2003	(first entry)
XX		

DE Murine, humanised Mu007 light chain variable region
XX

KM human interleukin (IL)-1 variable region, antibody, Crohn's disease;
KM human interleukin (IL)-1 β , anti-rheumatic; antiarthritis; humanised
KM anti-inflammatory; osteopathic; analgesic; cerebroprotective;
KM antihistaminic; immunosuppressive; antibacterial; vaccine; Muc07
KM rheumatoid arthritis; osteoarthritis; cartilage destruction; allergy;
KM septic shock; endotoxic shock; septicæmia, stroke; asthma;
KM graft versus host disease; inflammatory bowel disease.

Mus musculus
Synthetic.

PN WO2003010282-A2
XY

PD 06-FEB-2003
XX

18-JUL-2002; 2002WO-US021281.

26-JUL-2001; 2001US-0307973P
14-AUG-2001; 2001US-0312278P

(ELIL) LILLY & CO ELI.

Bright SN, Jia AY, Kuhstoss SA, Manetta JV, Tsurushita N,
PI Vasquez MJ;

WPI; 2003-248068/
N-PSDB; ABQ77443.

T New IL-1beta antibodies, useful for treating allergy, septic or endotoxemic shock, septicemia, stroke, asthma, graft versus host disease, Crohn's disease, or inflammatory bowel disease.

Disclosure; Page 70-71; 98pp; English.

This invention describes a novel antibody that specifically binds mature human interleukin (IL)-1beta, and binds the same epitope on mature human IL-1beta as mouse monoclonal antibody Mu007 or humanised antibody Hu007. The antibody of the invention have antiinflammatory, antiarthritic, antinflammatory, osteoprotective, antiallergic, cerebroprotective, antiaesthetic, immunosuppressive and antibacterial activity and can be used in a vaccine. The antibody is useful for manufacturing a medicament for treating rheumatoid arthritis or osteoarthritis, or for inhibiting cartilage destruction in a subject. The antibody is also useful for treating allergy, septic or endotoxemic shock, septicemia, stroke, graft versus host disease, Crohn's disease, or inflammatory bowel disease. This sequence represents the humanised murine Mu007 light chain variable region described in the disclosure of the invention.

Sequence 107 AA;

Query Match	91.6%;	Score 514;	DB 6;	Length 107;
Best Local Similarity	91.6%;	Pred. No. 2.5e-32;		
Matches	98;	Conservative	3;	Mismatches 6.

1 D I O M T S P S S L S A S V G D R V T I T C K A S Q D I N S Y L S W F Q Q K P G A P K T L I Y R A N R L V D G V P S 60

Db 1 DIQMTQSPSSLSASVGRVITITCKASQDIDRYLSWFOQKPGKAPKSLIYRVKRLVDGVPS 60
QY 61 RFSSGSGGQDYTLTSSIQPEDPATYTCLOYDEPPYTGSGTKVEIK 107
Db 61 RFSSGASGDTYTLTSSIQPEDPATYTCLOYDEPPYTGSGTKVEIK 107

RESULT 4
ABR83157
ID ABR83157 standard; protein; 107 AA.
XX
XX ABR83157;
XX AC
XX DT 15-JAN-2004 (first entry)
XX
XX Hu007 antibody light chain variable region sequence.
XX
XX Hu007; analogue; humanized antibody; IL-1beta; interleukin-1 beta;
XX complementarity determining region; osteopathic; antiarthritic;
XX gene therapy; CDR; human.
XX OS
XX Homo sapiens.
XX PN WO2003073982-A2.
XX PD 12-SEP-2003.
XX PF 20-FEB-2003; 2003WO-US003117.
XX PR 28-FEB-2002; 2002US-0361423P.
XX PA (ELIL) LILLY & CO ELI.
XX PI Beals JM, Huang L, Lu J, Rogers DP, Witcher DR,
XX WPI; 2003-731644/69.
XX DR
XX PT New analog of humanized antibody Hu007 that specifically binds mature IL-
PT 1 beta, useful for the manufacture of a medicament for treating
PT rheumatoid arthritis or osteoarthritis.
XX PS
XX Disclosure; Fig 1; 120pp; English.
XX CC The invention relates to an analogue of humanized antibody Hu007 that
CC specifically binds mature IL-1beta and comprises at least one amino acid
CC substitution at positions 54, 55 or 56 of the heavy chain complementarity
CC determining region 2 (CDR2). The analogue is useful for the manufacture
CC of a medicament for treating rheumatoid arthritis or osteoarthritis or
CC for inhibiting cartilage destruction. The present sequence represents an
CC antibody Hu007 light chain variable region
XX
SQ Sequence 107 AA;
Query Match 91.6%; Score 514; DB 7; Length 107;
Best Local Similarity 91.6%; Pred. No. 2.5e-32;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITITCKASQDIDRYLSWFOQKPGKAPKSLIYRVKRLVDGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITITCKASQDIDRYLSWFOQKPGKAPKSLIYRVKRLVDGVPS 60
QY 61 RFSSGSGGQDYTLTSSIQPEDPATYTCLOYDEPPYTGSGTKVEIK 107
Db 61 RFSSGASGDTYTLTSSIQPEDPATYTCLOYDEPPYTGSGTKVEIK 107

RESULT 5
ABG74711
ID ABG74711 standard; protein; 214 AA.
XX
XX AC ABG74711;
XX DT 10-MAY-2003 (first entry)

XX
DE Murine humanised Mu007 light chain variable region #2.
XX
XX Murine; light chain; variable region; antibody; Crohn's disease;
XX human interleukin (IL)-1beta; antirheumatic; antiarthritic; humanised;
XX antiinflammatory; osteopathic; antiallergic; cerebroprotective;
XX antiaesthetic; immunosuppressive; antibacterial; vaccine; Mu007;
XX rheumatoid arthritis; osteoarthritis; cartilage destruction; allergy;
XX septic shock; endotoxic shock; septicemia; stroke; asthma;
XX graft versus host disease; inflammatory bowel disease.
XX
XX Mus musculus.
XX OS
XX Synthetic.
XX PN WO2003010282-A2.
XX PD 06-FEB-2003.
XX PF 18-JUL-2002; 2002WO-US021281.
XX PR 26-JUL-2001; 2001US-0307973P.
XX PR 14-AUG-2001; 2001US-0312278P.
XX PA (ELIL) LILLY & CO ELI.
XX
XX Bright SM, Jia AY, Kuhstoss SA, Manetta JV, Tsurushita N;
XX Vaequez MJ;
XX WPI; 2003-248068/24.
XX DR N-PSDB; ABQ77444.
XX PS
XX PT New IL-1beta antibodies, useful for treating allergy, septic or endotoxic
PT shock, septicemia, stroke, asthma, graft versus host disease, Crohn's
PT disease, or inflammatory bowel disease.
XX
XX Disclosure; Page 75-76; 98pp; English.
XX
XX CC This invention describes a novel antibody that specifically binds mature
CC human interleukin (IL)-1beta, and binds the same epitope on mature human
CC IL-1beta as mouse monoclonal antibody Mu007 or humanized antibody Hu007.
CC The antibody of the invention have antirheumatic, antiallergic,
CC antiinflammatory, osteopathic, antiallergic, cerebroprotective,
CC antiaesthetic, immunosuppressive and antibacterial activity and can be
CC used in a vaccine. The antibody is useful for manufacturing a medicament
CC for treating rheumatoid arthritis or osteoarthritis, or for inhibiting
CC cartilage destruction in a subject. The antibody is also useful for
CC treating allergy, septic or endotoxic shock, septicemia, stroke, asthma,
CC graft versus host disease, Crohn's disease, or inflammatory bowel
CC disease. This sequence represents the humanised murine Mu007 light chain
CC variable region described in the disclosure of the invention
XX
SQ Sequence 214 AA;
Query Match 91.6%; Score 514; DB 6; Length 214;
Best Local Similarity 91.6%; Pred. No. 4.8e-32;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITITCKASQDIDRYLSWFOQKPGKAPKSLIYRVKRLVDGVPS 60
Db 1 DIQMTQSPSSLSASVGRVITITCKASQDIDRYLSWFOQKPGKAPKSLIYRVKRLVDGVPS 60
QY 61 RFSSGSGGQDYTLTSSIQPEDPATYTCLOYDEPPYTGSGTKVEIK 107
Db 61 RFSSGASGDTYTLTSSIQPEDPATYTCLOYDEPPYTGSGTKVEIK 107

RESULT 6
ABR83150
ID ABR83150 standard; protein; 214 AA.
XX
XX AC ABR83150;
XX DT 15-JAN-2004 (first entry)

XX Hu007 antibody analogue light chain sequence.
 DE
 XX
 KM Hu007; analogue; humanized antibody; IL-1beta; interleukin-1 beta;
 KM complementarity determining region; osteopathic; antiarthritic;
 KM gene therapy; CDR.
 XX
 OS Synthetic.
 XX
 PN WO2003073982-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 20-FEB-2003; 2003WO-US003117.
 XX
 PR 28-FEB-2002; 2002US-0361423P.
 XX
 PA (ELLY) LILLY & CO ELI.
 XX
 PI Beale JM, Huang L, Lu J, Rogers DP, Wicher DR,
 XX
 DR WPI; 2003-731644/69.
 DR N-PSDB; ACF57836.
 XX
 PT New analog of humanized antibody Hu007 that specifically binds mature IL-
 PT 1 beta, useful for the manufacture of a medicament for treating
 PT rheumatoid arthritis or osteoarthritis.
 XX
 PS Claim 17; Page 13-14; 120pp; English.
 XX
 CC The invention relates to an analogue of humanized antibody Hu007 that
 CC specifically binds mature IL-1beta and comprises at least one amino acid
 CC substitution at positions 54, 55 or 56 of the heavy chain complementarity
 CC determining region 2 (CDR2). The analogue is useful for the manufacture
 CC of a medicament for treating rheumatoid arthritis or osteoarthritis or
 CC for inhibiting cartilage destruction. The present sequence represents an
 CC antibody Hu007 analogue light chain sequence
 XX
 SQ Sequence 214 AA;
 Query Match 91.6%; Score 514; DB 7; Length 214;
 Best Local Similarity 91.6%; Pred. No. 4.8e-32;
 Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DIQMTGSPSSLSASVGDRTITCKASQDINSYLSWFOQKPGKAPKTLIYRANRLVDGVP 60
 DB 1 DIQMTGSPSSLSASVGDRTITCKASQDINSYLSWFOQKPGKAPKTLIYRANRLVDGVP 60
 QY 61 RFGSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTVEIK 107
 DB 61 RFGSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTVEIK 107
 RESULT 7
 AAR92082
 ID AAR92082 standard; protein; 107 AA.
 XX
 AC AAR92082;
 XX
 DT 16-OCT-2003 (revised)
 DT 15-MAY-1996 (first entry)
 XX
 DE Murine 1308F VL CDR-grafted K102 VL.
 XX
 KM Humanised antibody; chimeric antibody; antibody engineering;
 KM monoclonal antibody; Mab 1308F; respiratory syncytial virus; RSV;
 KM light chain; complementarity determining region; CDR.
 XX
 OS Homo; sapiens.
 OS Mus musculus.
 OS Chimeric.
 OS
 FH Key Location/Qualifiers

FT Region 24..34
 FT /label= CDR1
 FT Region 50..56
 FT /label= CDR2
 FT Region 89..97
 FT /label= CDR3
 XX
 PN WO9605229-A1.
 XX
 PD 22-FEB-1996.
 XX
 PF 09-AUG-1995; 95WO-US010053.
 XX
 PR 15-AUG-1994; 94US-00290592.
 XX
 PA (MED1-) MEDIMUNE INC.
 XX
 PI Johnson JS;
 XX
 DR WPI; 1996-139646/14.
 XX
 PT New chimeric antibodies against respiratory syncytial virus - comprise
 PT human antibodies with CDR's from the variable heavy and light chains of a
 PT murine antibody.
 XX
 PS Example 2; Fig 2A-2B; 55pp; English.
 XX
 CC A human-mouse chimeric antibody light chain has a human K102 framework
 CC contg. complementarity determining regions (CDRs) from the variable light
 CC (VL) chain of a murine monoclonal antibody (Mab 1308F) against
 CC respiratory syncytial virus (RSV) glycoprotein F antigenic site C. CDRs
 CC from Mab 1308 VL (AAR92083) were grafted into the human HV3 VL region
 CC (AAR92081) to produce CDR-grafted VL (AAR92082). A similar procedure was
 CC used to obtain CDR-grafted VH (AAR92079). The humanised antibody is used
 CC to treat RSV infection. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 107 AA;
 Query Match 90.9%; Score 510; DB 2; Length 107;
 Best Local Similarity 88.8%; Pred. No. 5e-32;
 Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DIQMTGSPSSLSASVGDRTITCKASQDINSYLSWFOQKPGKAPKTLIYRANRLVDGVP 60
 DB 1 DIQMTGSPSSLSASVGDRTITCKASQDINSYLSWFOQKPGKAPKTLIYRANRLVDGVP 60
 QY 61 RFGSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTVEIK 107
 DB 61 RFGSGSGGQDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTVEIK 107
 RESULT 8
 ABG31429
 ID ABG31429 standard; protein; 107 AA.
 XX
 AC ABG31429;
 XX
 DT 29-NOV-2002 (first entry)
 DT
 XX
 DE Humanised CDR-grafted anti-RSV F glycoprotein VL #1.
 XX
 KM Human-murine chimeric antibody; humanised antibody; CDR;
 KM complementarity determining region; variable heavy chain; VH;
 KM variable light chain; VL; monoclonal antibody; Mab; RSV infection;
 KM respiratory syncytial virus infection; vitruide; human; CDR-grafted;
 KM K102; anti-RSV F glycoprotein VL; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Synthetic.
 OS Chimeric.
 OS
 FH US2002102257-A1.

XX 01-AUG-2002.
PD
XX 21-SEP-1998; 98US-00158120.
PF
XX 21-SEP-1998; 98US-00158120.
PR
XX (JOHN/) JOHNSON L S.
PA
XX Johnson LS;
PI
XX WPI; 2002-673988/72.
DR
XX
XX New human-murine chimeric antibody useful for preventing or treating
PT respiratory syncytial viral (RSV) infection, contains at least one
PT complementarity determining region from a murine antibody.
PS
XX Example 2; Fig 2; 33pp; English.
PS
XX The present invention relates to a human-murine chimeric antibody
CC comprising a human antibody containing at least one complementarity
CC determining region (CDR) from each of the variable heavy (VH) and
CC variable light (VL) chains of a non-human, preferably murine, monoclonal
CC antibody (Mab) against respiratory syncytial virus (RSV). The humanised
CC antibody is useful for preventing or treating a respiratory syncytial
CC virus infection. The antibody is also useful for diagnosing RSV
CC infection. The antibody can be injected which is preferable to prior art
CC treatment methods involving intravenous transfusions. The present
CC sequence represents a human-murine chimeric antibody
XX
SQ Sequence 107 AA;

Query Match 90.9%; Score 510; DB 5; Length 107;
Best Local Similarity 88.8%; Pred. No. 5e-32;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGRVTITCKASQDINSYLSFWQKPKGKAPKTLIYRANRLVDGVP 60
DB 1 DIQWTQSPSSLSASVGRVTITCKASQDINSYLSFWQKPKGKAPKTLIYRANRLVDGVP 60
QY 61 RFSGSGGQDYTLTISLQPEDPATYVCLOYDEPPTFGGKTVEIK 107
DB 61 RFSGSGGTEFTLTISLQPEDPATYVCLOYDEPPTFGGKTVEIK 107

RESULT 9
AAR57482
ID AAR57482 standard; protein; 129 AA.
XX
AC AAR57482;
XX
DT 25-MAR-2003 (revised)
DT 02-OCT-1995 (first entry)
XX
DE Humanized 1308F VL.
XX
KW Monoclonal antibody; Mab; respiratory syncytial virus; RSV;
KW chimeric antibody; humanized antibody; antibody engineering; light chain;
KW VL; complementarity determining region; CDR.
XX
OS Synthetic.
XX
FH Key
FH Region
FT /label= CDR1
FT /label= CDR2
FT /label= CDR3
FT Region
XX
XX WO9417105-A1.
XX
XX 04-AUG-1994.

XX 29-JAN-1993; 93WO-US001168.
PF
XX 29-JAN-1993; 93WO-US001168.
PR
XX (MEDI-) MEDIMMUNE INC.
PA
XX Johnson L;
PI
XX WPI; 1994-264037/32.
DR
XX N-PSDB; AAQ67194.
DR
XX
XX Human-murine chimeric antibodies against respiratory syncytial virus -
PT comprises at least 1 CDR from each variable heavy and light chain of at
PT least 1 murine monoclonal antibody.
XX
XX Disclosure; Fig 4A-4B; 34pp; English.
PS
XX
XX Synthetic overlapping oligonucleotides and the 5' primer given in
CC AAQ67197 and 3' primer of AAQ67198 were used to construct a DNA sequence
CC (AAQ67194) encoding humanized 1308F VL (AAR57482) in which CDRs of the
CC anti-RSV F antigen murine Mab 1308F VL region were substituted into the
CC homologous human K102 gene. Similar procedures were used to obtain
CC humanized 1308F VH for the construction of anti-RSV F protein humanized
CC antibody. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 129 AA;

Query Match 90.9%; Score 510; DB 2; Length 129;
Best Local Similarity 88.8%; Pred. No. 6e-32;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQWTQSPSSLSASVGRVTITCKASQDINSYLSFWQKPKGKAPKTLIYRANRLVDGVP 60
DB 23 DIQWTQSPSSLSASVGRVTITCKASQDINSYLSFWQKPKGKAPKTLIYRANRLVDGVP 82
QY 61 RFSGSGGQDYTLTISLQPEDPATYVCLOYDEPPTFGGKTVEIK 107
DB 83 RFSGSGGTEFTLTISLQPEDPATYVCLOYDEPPTFGGKTVEIK 129

RESULT 10
AAR92085
ID AAR92085 standard; protein; 129 AA.
XX
AC AAR92085;
XX
DT 15-MAY-1996 (first entry)
DT
XX
DE Humanised antibody 1308 VL.
XX
KW Humanised antibody; chimeric antibody; antibody engineering;
KW monoclonal antibody; Mab 1308F; respiratory syncytial virus; RSV;
KW light chain; complementarity determining region; CDR.
XX
OS Synthetic.
XX
FH Key
FH Region
FT /label= CDR1
FT /label= CDR2
FT /label= CDR3
FT Region
XX
XX WO9605229-A1.
XX
XX 22-FEB-1996.
XX
XX 09-AUG-1995; 95WO-US010053.
XX
XX 15-AUG-1994; 94US-00290592.
XX

PA (MEDI-) MEDIMUNE INC.
XX Johnson LS;
XX
DR WPI, 1996-139646/14.
DR N-PSDB, AAT16181.
XX
XX New chimeric antibodies against respiratory syncytial virus - comprise
PT human antibodies with CDR's from the variable heavy and light chains of a
PT murine antibody.
PS Example 2, Fig 4A-4B; 55pp; English.
XX
XX A human-mouse chimeric antibody light chain has a human HV3 framework
CC contg. complementarity determining regions (CDRs) from the variable light
CC (VL) chain of murine monoclonal antibody (Mab) 1308P active against
CC respiratory syncytial virus (RSV) glycoprotein F antigenic site C. DNA
CC (AAT16181) coding for CDR-grafted VL-encoding region, Hui308 VL
CC (AAR92085), was synthesized using overlapping oligonucleotides. The
CC construct was used with Hui308 VH (see AAR92084) for prodn. in COS-1
CC transfectants of humanised antibody useful for treatment of RSV infection
CC
SQ Sequence 129 AA;
Query Match 90.9%; Score 510; DB 2; Length 129;
Best Local Similarity 88.8%; Pred. No. 6e-32;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVTTCRASODINYSWFOQKPGKAPKTLTYRANRLVDGVP 60
DB 23 DIQMTSPSTLSASVGDRTVTTCRASODINRYLMWYQKPGKAPKTLTYRANRLVDGVP 82
QY 61 RFSGSGSGQDYTLTISLQPEDPATYCYQYDEFPYFGGTYEIK 107
DB 83 RFSGSGSGTEFTLTISLQPDPAFYCYQYFHEFPYFGGTYEIK 129
RESULT 11
ABG31444
ID ABG31444 standard; protein, 129 AA.
AC ABG31444;
XX
DT 29-NOV-2002 (first entry)
XX
XX Amino acid sequence for humanised antibody Hui308VL.
XX
XX Human-murine chimeric antibody; humanised antibody; CDR;
KW complementarity determining region; variable heavy chain; VH;
KW variable light chain; VL; monoclonal antibody; Mab; RSV infection;
KW respiratory syncytial virus infection; virucide; Hui308VL; mutant;
KW muteln.
XX
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
OS
XX US2002102257-A1.
XX
XX 01-AUG-2002.
XX
XX 21-SEP-1998; 98US-00158120.
XX
XX 21-SEP-1998; 98US-00158120.
XX
XX (JOHN/) JOHNSON L S.
XX
XX Johnson LS;
XX
XX WPI, 2002-673988/72.
XX
XX New human-murine chimeric antibody useful for preventing or treating

PT respiratory syncytial viral (RSV) infection, contains at least one
PT complementarity determining region from a murine antibody.
XX
XX Example 2, Fig 4; 33pp; English.
XX
XX The present invention relates to a human-murine chimeric antibody
CC comprising a human antibody containing at least one complementarity
CC determining region (CDR) from each of the variable heavy (VH) and
CC variable light (VL) chains of a non-human, preferably murine, monoclonal
CC antibody (Mab) against respiratory syncytial virus (RSV). The humanised
CC antibody is useful for preventing or treating a respiratory syncytial
CC virus infection. The antibody is also useful for diagnosing RSV
CC infection. The antibody can be injected which is preferable to prior art
CC treatment methods involving intravenous transfusions. The present
CC sequence represents a human-murine chimeric antibody
CC
SQ Sequence 129 AA;
Query Match 90.9%; Score 510; DB 5; Length 129;
Best Local Similarity 88.8%; Pred. No. 6e-32;
Matches 95; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVTTCRASODINYSWFOQKPGKAPKTLTYRANRLVDGVP 60
DB 23 DIQMTSPSTLSASVGDRTVTTCRASODINRYLMWYQKPGKAPKTLTYRANRLVDGVP 82
QY 61 RFSGSGSGQDYTLTISLQPEDPATYCYQYDEFPYFGGTYEIK 107
DB 83 RFSGSGSGTEFTLTISLQPDPAFYCYQYFHEFPYFGGTYEIK 129
RESULT 12
AAM58478
ID AAM58478 standard; protein, 107 AA.
AC AAM58478;
XX
XX 18-AUG-1998 (first entry)
XX
XX Humanised anti-CD5 immunoglobulin H65 light chain variable region #1.
XX
XX Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW depletion; cytotoxic; immunconjugate; fusion protein; psoriasis;
KW autoimmune disease; rheumatoid arthritis; type I diabetes.
XX
XX Synthetic.
OS Mus sp.
OS Homo sapiens.
OS
XX US5770196-A.
XX
XX 23-JUN-1998.
XX
XX 07-JUN-1995; 95US-00472788.
XX
XX 13-DEC-1991; 91US-00808464.
XX
XX 14-DEC-1992; 92WO-US010906.
XX
XX 23-JUN-1993; 93US-00082842.
XX
XX (XOMA) XOMA CORP.
XX
XX Studnicka GM;
XX
XX WPI, 1998-376744/32.
XX
XX Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies with
PT humanised variable regions.
XX
XX Claim 1; Col 63-64; 77pp; English.
XX
XX A method has been developed of depleting CD5+ cells in an animal. The
CC method comprises administering a cytotoxic protein containing a modified
CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig

CC molecule or an immunoglobulin or fusion protein containing an anti-CD5
 CC Ig molecule, and where the modified Ig variable domain comprises at least
 CC one of (a) a modified light chain variable region (see AAM58478 or
 CC AAM58480), and (b) a modified heavy chain variable region (see AAM58479
 CC or AAM58481), where AAM58478 and AAM58479 are humanised forms of the H65
 CC light and heavy chain variable domains with low risk amino acid
 CC substitutions [i.e. low risk of reducing antigen-binding specificity].
 CC and AAM58480 and AAM58481 are humanised forms of the H65 light and heavy
 CC chain variable domains with moderate risk amino acid substitutions and
 CC are present in humanised H65 antibody H63 (ATCC HB 11206). The method is
 CC useful for treating autoimmune diseases, especially systemic lupus
 CC erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The
 CC present sequence represents a specifically claimed humanised anti-CD5
 CC immunoglobulin H65 light chain variable region
 CC
 SQ Sequence 107 AA;
 Query Match 89.5%; Score 502; DB 2; Length 107;
 Best Local Similarity 88.8%; Pred. No. 2.1e-31;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINSYLSWFOQKPKKPKTLIYRANRLVDGVP 60
 Db 1 DIQMTQSPSSLSASVGRVITTCRASQDINSYLSWFOQKPKKPKTLIYRANRLVDGVP 60
 QY 61 RFSGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTVEIK 107
 Db 61 RFSGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTVEIK 107
 RESULT 13
 AD101168
 ID AD101168 standard; protein; 107 AA.
 AC AD101168;
 XX
 DT 22-APR-2004 (first entry)
 DE Murine monoclonal antibody H65 humanised light chain VL protein 1.
 XX
 KW variable domain; immunosuppressive; dermatological; antiinflammatory;
 KW antidiabetic; antichryoid; antiporiatic; antirheumatic; antiarthritic;
 KW neuroprotective; antineur; antianaemic; fungicide; virucide; autolimmune;
 KW systemic lupus erythematosus; lupus nephritis; scleroderma; morphea;
 KW lichen planus; rheumatoid arthritis; spondylarthritis; thyroiditis;
 KW pemphigus vulgaris; diabetes mellitus type 1;
 KW progressive systemic sclerosis; aplastic anaemia; myasthenia gravis;
 KW myositis; polymyositis; dermatomyositis; Sjogren's disease;
 KW collagen vascular; polyarteritis; inflammatory bowel; Crohn's;
 KW ulcerative colitis; multiple sclerosis; psoriasis;
 KW primary biliary cirrhosis; T cell; tissue transplant rejection;
 KW graft versus host disease; viral; fungal infection; murine; mouse;
 KW monoclonal antibody; H65; humanised light chain.
 XX
 OS Mus sp.
 OS Synthetic.
 OS
 PN US2003229207-A1.
 PD 11-DEC-2003.
 PF 10-JAN-2003; 2003US-00340189.
 XX
 PR 13-DEC-1991; 91US-00808464.
 PR 14-DEC-1992; 92MO-US010906.
 PR 23-JUN-1993; 93US-00082842.
 PR 05-FEB-1999; 99US-00245202.
 XX
 PA (XOMA) XOMA TECHNOLOGY LTD.
 XX
 PI Studnicka GM;
 XX
 DR WPI; 2004-042226/04.

XX
 PT Novel protein containing modified variable domain comprising amino acid
 PT sequence modified at low risk positions in heavy or light chain amino
 PT acid residue at corresponding position of native antibody sequence.
 XX
 PS -Example 6; SEQ ID NO 27; 80pp; English.
 XX
 CC The invention relates to a novel protein containing a modified variable
 CC domain comprising an amino acid sequence modified at low risk positions
 CC such that each amino acid residue in a low risk position in the light or
 CC heavy chain variable region sequence of the domain is same as the amino
 CC acid residue at the corresponding position of a selected antibody light
 CC or heavy chain variable region sequence or consensus sequence. The
 CC polypeptide of the invention demonstrates immunosuppressive,
 CC dermatological, antiinflammatory, antidiabetic, antichryoid,
 CC antiporiatic, antirheumatic, antiarthritic, neuroprotective, antineur,
 CC antianaemic, fungicide and virucide activities. The polypeptide may be
 CC useful for treating autoimmune diseases including systemic lupus
 CC erythematosus and lupus nephritis, scleroderma including morphea and
 CC lichen planus, rheumatoid arthritis and spondylarthritis, thyroiditis,
 CC pemphigus vulgaris, diabetes mellitus type 1, progressive systemic
 CC sclerosis, aplastic anaemia, myasthenia gravis, myositis including
 CC polymyositis and dermatomyositis, Sjogren's disease, collagen vascular
 CC disease, polyarteritis, inflammatory bowel disease including Crohn's
 CC disease and ulcerative colitis, multiple sclerosis, psoriasis and primary
 CC biliary cirrhosis. Furthermore, the polypeptide may be utilised to
 CC address other diseases mediated by T cells, such as tissue transplant
 CC rejection and graft versus host disease, as well as diseases caused by
 CC viral or fungal infection. The current sequence is that of the murine
 CC antibody variable domain protein of the invention.
 CC
 SQ Sequence 107 AA;
 Query Match 89.5%; Score 502; DB 8; Length 107;
 Best Local Similarity 88.8%; Pred. No. 2.1e-31;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINSYLSWFOQKPKKPKTLIYRANRLVDGVP 60
 Db 1 DIQMTQSPSSLSASVGRVITTCRASQDINSYLSWFOQKPKKPKTLIYRANRLVDGVP 60
 QY 61 RFSGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTVEIK 107
 Db 61 RFSGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYTFGGGTVEIK 107
 RESULT 14
 AA552724
 ID AA552724 standard; protein; 107 AA.
 AC AA552724;
 XX
 DT 26-JAN-2000 (first entry)
 DE Humanised ATR-5 L chain V region version "b1" protein sequence.
 XX
 KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
 KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; chromoblastic disease; DIC;
 KW disseminated intravascular coagulation; immunogenicity; chimeric.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS
 PN WO9951743-A1.
 PD 14-OCT-1999.
 PF 02-APR-1999; 99MO-JP001768.
 PR 03-APR-1998; 98JP-00091850.
 XX
 PA (CHUGAI) CHUGAI SEIYAKU KK.
 XX

PI Sato K, Adachi H, Yabuta N;
 XX
 DR WPI; 1999-620204/53.
 DR N-PSDB; AA233089.
 PT Humanised antibody recognizing human tissue factor, used for treatment of
 PT disseminated intravascular coagulation.
 XX
 PS Claim 18; Page 259; 291pp; Japanese.
 CC The present invention describes chimeric antibody (Ab) heavy (H) chains
 CC containing the variable region of the H chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hrp) and the constant region of the H
 CC chain of a human Ab. The variable region is one of six specified
 CC sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
 CC containing the variable region of the L chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hrp) and the constant region of the L
 CC chain of a human Ab, the variable region being one of six specified
 CC sequences (which are the L chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
 CC and prevention of thrombotic disease, especially of disseminated
 CC intravascular coagulation (DIC). The humanised antibody has the high hrp
 CC binding activity of the mouse monoclonal antibody but greatly reduced
 CC immunogenicity. AA233001 to AA233091 and Y527007 to AY52767 represent
 CC sequences used in the exemplification of the present invention
 CC
 XX
 SQ Sequence 107 AA;

Query Match 88.9%; Score 499; DB 2; Length 107;
 Best Local Similarity 89.7%; Pred. No. 3.5e-31;
 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTVITCKASQDINSYLSWFOQKPGKAPKTLITRANRLVDGVPS 60
 DB 1 DIQMTQSPSSLSASVDGRTVITCKASQDINSYLSWFOQKPGKAPKTLITRANRLVDGVPS 60
 QY 61 RFSGSGSGQDYTLTISSLOPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
 DB 61 RFSGSGSGQDYTLTISSLOPEDFATYYCLQYDEFPYTFGGGTKVEIK 107

RESULT 15
 AAB74985
 ID AAB74985 standard; protein; 107 AA.
 AC AAB74985;
 XX
 DT 16-JUL-2001 (first entry)

DE Humanised ATR-5 L chain V region version b1 SEQ ID NO:96.
 XX
 XX Mouse; human; humanised; monoclonal antibody; tissue factor; TF;
 KW prevention; blood coagulation; tumour; ATR-5; anticoagulant;
 KW thrombolytic; infection; venous thrombosis; arterial thrombosis;
 KW vascular medial thickening; accelerated blood coagulation; thrombosis;
 XX blood vessel thickening.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS
 XX
 PN MO200124626-A1.
 PD 12-APR-2001.

PF 29-SEP-2000; 2000MO-JP06802.
 XX
 PR 01-OCT-1999; 99JP-00281843.
 PR 01-OCT-1999; 99JP-00282120.
 PR 01-OCT-1999; 99JP-00282134.
 PR 01-OCT-1999; 99JP-00282167.
 PR 01-OCT-1999; 99JP-00282188.
 PR 01-OCT-1999; 99JP-00282192.

XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Saito H, Kitazawa T, Yoshihashi K, Hattori K;
 XX
 DR WPI; 2001-300135/31.
 DR N-PSDB; AAF87914.
 XX
 PT Mouse model for sustained accelerated blood coagulation and treatment for
 PT accelerated blood coagulation, thrombosis and blood vessel thickening.
 XX
 PS Example; Page 186-187; 202pp; Japanese.

CC The present invention describes an experimental animal model transplanted
 CC with animal cells expressing human tissue factor or a fragment of it,
 CC with accelerated blood coagulation. Also described are: (1) selecting an
 CC animal model; (2) screening for anti-thrombotics; (3) treatment and
 CC prevention of accelerated blood coagulation; and (4) polyclonal and
 CC monoclonal antibodies or their fragments. The animal model is useful in
 CC the search and development of remedies for diseases associated with the
 CC sustained acceleration of blood coagulation such as that caused by
 CC infection, venous thrombosis, arterial thrombosis and disease caused by
 CC vascular medial thickening. Antibodies from the present invention against
 CC human tissue factor (TF) (e.g. anti mouse monoclonal antibody ATR-5 and
 CC humanised ATR-5) can be used in the treatment and prevention of
 CC accelerated blood coagulation, thrombosis and blood vessel thickening.
 CC AAF87837 to AAF87917 and AAB74968 to AAB74990 represent nucleotide and
 CC protein sequences which are used in the exemplification of the present
 CC invention
 CC
 XX
 SQ Sequence 107 AA;

Query Match 88.9%; Score 499; DB 4; Length 107;
 Best Local Similarity 89.7%; Pred. No. 3.5e-31;
 Matches 96; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTVITCKASQDINSYLSWFOQKPGKAPKTLITRANRLVDGVPS 60
 DB 1 DIQMTQSPSSLSASVDGRTVITCKASQDINSYLSWFOQKPGKAPKTLITRANRLVDGVPS 60
 QY 61 RFSGSGSGQDYTLTISSLOPEDFATYYCLQYDEFPYTFGGGTKVEIK 107
 DB 61 RFSGSGSGQDYTLTISSLOPEDFATYYCLQYDEFPYTFGGGTKVEIK 107

Search completed: December 29, 2004, 17:57:35
 Job time : 74.5428 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:38:43 ; Search time 73.8584 Seconds
(without alignments)
833.556 Million cell updates/sec

Title: US-10-774-076-14

Perfect score: 561

Sequence: 1 DIQMTQSPSSLSASVDGRVT.....CLQYDEPPYFGSGTKVERK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_02:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	494	88.1	214	2 Q9RIA5	Q9RIA5 mus musculu
2	494	88.1	236	2 Q7S98	Q7S98 mus musculu
3	474	84.5	128	1 KV5E_MOUSE	P01637 mus musculu
4	449	80.0	108	1 KV1Y_HUMAN	P03362 homo sapien
5	446	79.5	236	2 Q7Z3Y4	Q7Z3Y4 homo sapien
6	445	79.3	236	2 Q6GMX8	Q6GMX8 homo sapien
7	444	79.1	108	1 KV1B_HUMAN	P01594 homo sapien
8	444	79.1	236	2 Q7TWK3	Q7TWK3 mus musculu
9	443	79.0	108	1 KV1V_HUMAN	P04430 homo sapien
10	442	78.8	108	1 KV1P_HUMAN	P01608 homo sapien
11	442	78.8	115	1 KV5F_MOUSE	P01638 mus musculu
12	441	78.6	108	1 KV1R_HUMAN	P01610 homo sapien
13	439	78.3	108	1 KV1O_HUMAN	Q6GMX9 homo sapien
14	437	77.9	236	2 Q6GMX9	Q6GMX9 homo sapien
15	436.5	77.8	107	2 Q96SA9	Q96SA9 homo sapien
16	435	77.5	108	2 Q9UL70	Q9UL70 homo sapien
17	435	77.5	236	2 Q6PIH7	Q6PIH7 homo sapien
18	435	77.5	236	2 Q6GMW1	Q6GMW1 homo sapien
19	435	77.5	236	2 AAH34141	AAH34141 homo sapi
20	433	77.2	108	2 Q9UL77	Q9UL77 homo sapien
21	432	77.0	108	1 KV1H_HUMAN	P01600 homo sapien
22	432	77.0	236	2 Q6GMX0	Q6GMX0 homo sapien
23	427.5	76.2	107	1 KV1D_HUMAN	P01596 homo sapien
24	427	76.1	108	1 KV1A_HUMAN	P01599 homo sapien
25	427	76.1	108	1 KV1M_HUMAN	P01605 homo sapien
26	427	75.9	108	1 KV1L_HUMAN	P01604 homo sapien
27	426	75.9	108	1 KV1S_HUMAN	P01611 homo sapien
28	423	75.4	108	1 KV1E_HUMAN	P01597 homo sapien
29	420	74.9	108	1 KV1F_HUMAN	P01598 homo sapien
30	420	74.9	108	1 KV1Q_HUMAN	P01609 homo sapien
31	419	74.7	108	1 KV1Q_HUMAN	P01609 homo sapien

32	418	74.5	108	1 KV1C_HUMAN	P01595 homo sapien
33	416	74.2	129	1 KV1X_HUMAN	P04432 homo sapien
34	414	73.8	108	1 KV1Z_HUMAN	P01603 homo sapien
35	414	73.8	108	2 Q9UL79	Q9UL79 homo sapien
36	413	73.6	234	2 Q7Z473	Q7Z473 homo sapien
37	408	72.7	129	1 KV1W_HUMAN	P04431 homo sapien
38	403	71.8	108	1 KV1N_HUMAN	P01606 homo sapien
39	403	71.8	236	2 Q6PIT5	Q6PIT5 homo sapien
40	403	71.8	236	2 AAH29444	AAH29444 homo sapi
41	402.5	71.7	107	2 Q9UL81	Q9UL81 homo sapien
42	402	71.7	116	2 Q96PF6	Q96PF6 homo sapien
43	402	71.7	236	2 Q6PIH4	Q6PIH4 homo sapien
44	402	71.7	236	2 AAH34146	AAH34146 homo sapi
45	401	71.5	108	1 KV5T_MOUSE	P01653 mus musculu

ALIGNMENTS

RESULT 1	ID	Q9RIA5	P01637	214 AA.
AC	Q9RIA5	P01637	214 AA.	
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Kappa light chain of Mab7 (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.,			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF152371; AAD40242.1; -			
DR	PIR; PH1065; PH1065.			
DR	PDB; 1AHW; X-ray; D=-			
DR	PDB; 1CTC; X-ray; A/C=1-214.			
DR	PDB; 1E08; X-ray; -			
DR	PDB; 1K6Q; X-ray; L=1-210.			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:0006355; P:regulation of transcription factor activity; IEA.			
DR	InterPro; IPR001356; Homeobox.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG_c1.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF07654; C1-set; I.			
DR	Pfam; PF00647; Ig; I.			
DR	PRINTS; PR00024; HOMEBOX.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PSS0835; IG_LIKE; 2.			
DR	PROSITE; PSS0290; IG_MHC; UNKNOWN_1.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE 214 AA; 23922 MW; 52BA205FDE9552A CRC64;			
Query Match	88.1%; Score 494; DB 2; Length 214;			
Best Match Similarity	86.0%; Pred. No. 3.5e-43;			
Matches	92; Conservative 9; Mismatches 6; Indels 0; Gaps 0;			
QY	1 DIQMTQSPSSLSASVDGRVTITCKASQDINSYLSWFOQKPKGAKPTLIYRANLVGVPS 60			
DB	1 DIQMTQSPSSLSASVDGRVTITCKASQDINSYLSWFOQKPKGAKPTLIYRANLVGVPS 60			
QY	61 RESGSGSGQDYTLTISLSLOPEDPATYTCLOYDEPPYFGSGTKVERK 107			
DB	61 RESGSGSGQDYTLTISLSLEEDMGITYCLOYDEPPYFGSGTKVERK 107			
RESULT 2				

Q7TS98
ID Q7TS98 PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93383497; PubMed=8372513;
RA Tonge D.W., Henman J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 116NS19.9 heavy and light chain
cDNAs and expression of antibody fragments in Escherichia coli.";
RL Year Immunol. 7:56-62(1993).
DR EMBL; S65921; AAB28160.1;-
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; I.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 26454 MW; 2C586BF5EA10F4C CRC64;

Query Match 88.1%; Score 494; DB 2; Length 236;
Best Local Similarity 86.9%; Pred. No. 3.9e-43;
Matches 93; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITCKASODINSYLSMFOCKPKGAKPTLIYRANRLVDGVS 60
DB 23 DIKMTQSPSSMYASIGERVITTCASODINSYLSMFOCKPKSKPTLIYRANRLVDGVS 82
QY 61 RFSSGSGSQDYTLTITSLQPEDFATYTCLOYDEFPYTPGGGTKEIK 107
DB 83 RFSSGSGSQDYTLTITSLLEYEDMGIIYCYLQYDEFPPTFGGTKEIK 129

RESULT 3
KVSE MOUSE
ID KVSE MOUSE STANDARD; PRT; 128 AA.
AC P01637;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region T1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81052342; PubMed=6776411;
RA Altenburger W., Steinmetz M., Zachau H.G.;
RT "Functional and non-functional joining in immunoglobulin light chain
genes of a mouse myeloma.";
RL Nature 287:603-607(1980).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL; V00072; CAA24150.1; -
DR PIR; A01920; KVMSTL.

DR HSPB; P80362; 1WTU.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 Ig kappa chain V-V region T1.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 54 Complementarity-determining-1.
FT DOMAIN 55 69 Framework-2.
FT DOMAIN 70 76 Complementarity-determining-2.
FT DOMAIN 77 108 Framework-3.
FT DOMAIN 109 117 Complementarity-determining-3.
FT DOMAIN 118 127 Framework-4.
FT DISULFID 43 108 By similarity.
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14385 MW; AFA5563D31BB7E05 CRC64;

Query Match 84.5%; Score 474; DB 1; Length 128;
Best Local Similarity 81.3%; Pred. No. 2.3e-41;
Matches 87; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTITCKASODINSYLSMFOCKPKGAKPTLIYRANRLVDGVS 60
DB 21 DIKMTQSPSSMYASIGERVITTCASODINSYLSMFOCKPKSKPTLIYRANRLVDGVS 80
QY 61 RFSSGSGSQDYTLTITSLQPEDFATYTCLOYDEFPYTPGGGTKEIK 107
DB 81 RFSSGSGSQDYTLTITSLLEYEDMGIIYCYLQYDEFPPTFGGTKEIK 127

RESULT 4
KVLY HUMAN
ID KVLY HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=793911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RT Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origins of altered domain interactions in immunoglobulin
RT light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RT Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human K1 Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -----
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1WTL; X-ray; A/B=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KM 3D-structure; Bence-Jones protein; Direct protein sequencing;

Immunoglobulin V region.

KT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT CONFLICT 30 31 TN -> SD (in Ref. 2).
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 45 49
 FT STRAND 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT STRAND 80 82
 FT HELIX 84 90
 FT STRAND 98 98
 FT STRAND 102 106
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 80.0%; Score 449; DB 1; Length 108;
 Best Local Similarity 79.4%; Pred. No. 7.7e-39;
 Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSAVGDRVTTCASODINSYLSWFOOKPKKPTIYRANRLVDGVP 60
 Db 1 DIQMTQSPSSLSAVGDRVTTCASODINSYLSWFOOKPKKPTIYRANRLVDGVP 60

QY 61 RFGSGSGGDYTTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 Db 61 RFGSGSGGDYTTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107

RESULT 5

Q723Y4 PRELIMINARY; PRT; 236 AA.

ID Q723Y4
 AC Q723Y4
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal Muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal Muscle;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005332; AA005332.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25702 MW; 7EBFE4ED23084BC6 CRC64;

Query Match 79.5%; Score 446; DB 2; Length 236;
 Best Local Similarity 79.4%; Pred. No. 3.9e-38;
 Matches 85; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSAVGDRVTTCASODINSYLSWFOOKPKKPTIYRANRLVDGVP 60
 Db 23 DIQMTQSPSSLSAVGDRVTTCASODINSYLSWFOOKPKKPTIYRANRLVDGVP 60

QY 61 RFGSGSGGDYTTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 Db 83 RFGSGSGGDYTTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 129

RESULT 6

Q6GKX8 PRELIMINARY; PRT; 236 AA.

ID Q6GKX8
 AC Q6GKX8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC073764; AAH73764.1; -
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_2.
 DR Pfam; PF07654; C1-secl; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Hypothetical protein.
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 79.3%; Score 445; DB 2; Length 236;
 Best Local Similarity 79.4%; Pred. No. 5e-38;
 Matches 85; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 Oy 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKKTLIRANLVDSGPS 60
 Db 23 DIQMTQSPSSVSAVSGRVTITCRASQGISWLAWQQRGKAPKLLIYASNSLGSVPS 82
 Oy 61 RFGSGSGQDYTLTISLQPEDPATYTCQYDEFPYFGGTYVEIK 107
 Db 83 RFGSGSGQDYTLTISLQPEDPATYTCQYDEFPYFGGTYVEIK 129

RESULT 7

KV1B_HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 1-OCT-2004 (Rel. 45, Last annotation update)
 DE IG kappa chain V-1 region AD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hilemann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehlehammer H., Schliffer M., Epp O., Colman P.M., Lattman E.E.,
 RT Schwaeger P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the Bence-
 Jones protein Au.";
 RL Jones protein Au.";
 RT Jones protein Au.";
 CC -1- MISCELLANEOUS: The structure of the V region was determined by
 molecular replacement methods using the known structure of the V
 region of the kappa chain REI.
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 DR PIR; A91653; KIHUV.
 DR PDB; 1UV5; X-ray; A=1-107.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KV Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT STRAND 4 5
 FT STRAND 10 13
 FT STRAND 15 16
 FT STRAND 19 25
 FT STRAND 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 44 49
 FT TURN 50 52
 FT STRAND 53 54
 FT STRAND 55 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT STRAND 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E801187BE6FEF9 CRC64;
 Query Match 79.1%; Score 444; DB 1; Length 108;
 Best Local Similarity 79.4%; Pred. No. 2.5e-38;
 Matches 85; Conservative 7; Mismatches 15; Indels 0; Gaps 0;
 Oy 1 DIQMTQSPSSLSASVGRVTITCKASQDINSYLSWFOQKPKKTLIRANLVDSGPS 60
 Db 1 DIQMTQSPSSLSASVGRVTITCKASQDISYLSWFOQKPKKTLIYASNSLGSVPS 60
 Oy 61 RFGSGSGQDYTLTISLQPEDPATYTCQYDEFPYFGGTYVEIK 107
 Db 61 RFGSGSGAHFTTISLQPEDPATYTCQYDYLPYFGGTYVEIK 107

RESULT 8

07TMK3 PRELIMINARY; PRT; 236 AA.
 AC 07TMK3;
 DT 01-OCT-2003 (TRENBERL. 25, Created)
 DT 01-OCT-2003 (TRENBERL. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBERL. 26, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carrinzi P., Prange C.,
 RA Rata S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatacne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C2ECH 11;
 RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
 RA Straube R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC055906; AAH55906.1;
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig-MHC.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF07654; Cl-bet; I.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IgV; I.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KM Hypothetical protein_
 SQ SEQUENCE 236 AA; 26299 MW; 0DB03488AA6396F CRC64;

Query Match 79.1%; Score 444; DB 2; Length 236;
 Best Local Similarity 78.5%; Pred. No. 6.3e-38;
 Matches 84; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 23 DIKWTGSPSSMYSLGKRVITTCASQDINSYLSWYQOKPKKTLIYATSLADGVP 82
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 83 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 129

RESULT 9
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P04430;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region BAN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=66174817; Pubmed=3083240;
 RA Druet P.E., O'Connor T.P., Benson M.D., amyloid protein (BAN).";
 RT "Polynorphin in a kappa I primary (AL) amyloid protein (BAN).";
 RL M01. Immunol. 23:73-78(1986).
 DR PIR; A01878; KIHUBN.
 DR HSP; P80362; IWTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.

DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Amyloid; Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 61 NFGSGSGGTFTLITSLQPEDPATYTCQYNGVPYFGGTVEIK 107

RESULT 10
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=68362076; Pubmed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RN REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnickol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
 RL York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91638; KIHURY.
 DR HSP; P01607; IBMW.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 61 NFGSGSGGTFTLITSLQPEDPATYTCQYNGVPYFGGTVEIK 107

RESULT 10
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=68362076; Pubmed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RN REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnickol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
 RL York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91638; KIHURY.
 DR HSP; P01607; IBMW.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 61 NFGSGSGGTFTLITSLQPEDPATYTCQYNGVPYFGGTVEIK 107

RESULT 10
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=68362076; Pubmed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RN REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnickol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
 RL York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91638; KIHURY.
 DR HSP; P01607; IBMW.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 61 NFGSGSGGTFTLITSLQPEDPATYTCQYNGVPYFGGTVEIK 107

RESULT 10
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=68362076; Pubmed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RN REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnickol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
 RL York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91638; KIHURY.
 DR HSP; P01607; IBMW.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 61 NFGSGSGGTFTLITSLQPEDPATYTCQYNGVPYFGGTVEIK 107

RESULT 10
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=68362076; Pubmed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RN REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnickol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
 RL York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91638; KIHURY.
 DR HSP; P01607; IBMW.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 61 NFGSGSGGTFTLITSLQPEDPATYTCQYNGVPYFGGTVEIK 107

RESULT 10
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=68362076; Pubmed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RN REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnickol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
 RL York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91638; KIHURY.
 DR HSP; P01607; IBMW.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 61 NFGSGSGGTFTLITSLQPEDPATYTCQYNGVPYFGGTVEIK 107

RESULT 10
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=68362076; Pubmed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RN REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnickol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
 RL York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91638; KIHURY.
 DR HSP; P01607; IBMW.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 61 NFGSGSGGTFTLITSLQPEDPATYTCQYNGVPYFGGTVEIK 107

RESULT 10
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=68362076; Pubmed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RN REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnickol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
 RL York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91638; KIHURY.
 DR HSP; P01607; IBMW.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 DB 1 DIQWTGSPSSLSASVGDRTTTCASQDINSYLSWFOQKPKAKTLIRANRLVDGVP 60
 QY 61 RFGSGSGGDYTLTISLQPEDPATYTCLOYDEFPYFGGTVEIK 107
 DB 61 NFGSGSGGTFTLITSLQPEDPATYTCQYNGVPYFGGTVEIK 107

RESULT 10
 KVIH HUMAN STANDARD; PRT; 108 AA.
 AC P01608;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP MEDLINE=68362076; Pubmed=5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 RT Cum.).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RN REVISIONS TO 39 AND 41.
 RA Hilschmann N., Barnickol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
 RL York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 CC marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A91638; KIHURY.
 DR HSP; P01607; IBMW.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; Ig; I.
 DR SMART; SM00406; IG; I.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DISULFID 23 88
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FB96FD37 CRC64;

Query Match 79.0%; Score 443; DB 1; Length 108;
 Best Local Similarity 76.6%; Pred. No. 3.2e-38;
 Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQWTGSPSSLSASVGDRT

FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11782 MW; 55ACEDESA313DF3A CRC64;

Query Match 78.8%; Score 442; DB 1; Length 108;
 Best Local Similarity 77.6%; Pred. No. 4.1e-38;
 Matches 83; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQDINSYLSWFQKRGKAPKTLIYRANRLVDGVPS 60
 DB 1 DIOMTQSPSSLSASVGDRTVITTCASQDINSYLSWFQKRGKAPKTLIYRANRLVDGVPS 60
 QY 61 RFSGSGSGDYTLTISLQPEDPATYTCQYDEFPYTFGSGTKVEIK 107
 DB 61 RFSGSGSGDYTLTISLQPEDPATYTCQYDEFPYTFGSGTKVEIK 107

QY 61 RFSGSGSGDYTLTISLQPEDPATYTCQYDEFPYTFGSGTKVEIK 107
 DB 61 RFSGSGSGDYTLTISLQPEDPATYTCQYDEFPYTFGSGTKVEIK 107

RESULT 11

KVIF_MOUSE

ID KVIF_MOUSE STANDARD; PRT; 115 AA.

AC P01638;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region 16 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81220975; PubMed=6264318;
 RA Rech M., Hochel J., Schnell H., Zachau H.G.;
 RT "Differences between germ-line and rearranged immunoglobulin V kappa
 RT coding sequences suggest a localized mutation mechanism."
 RL Nature 291:668-670(1981).
 DR PIR; A01921; KBW6.
 DR HSSP; P01607; 1BWW.
 DR InterPro; IPR007110; Ig-1-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 20
 FT DOMAIN 21 43 Ig kappa chain V-V region 16.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 54 Complementarity-determining-1.
 FT DOMAIN 55 69 Framework-2.
 FT DOMAIN 70 76 Complementarity-determining-2.
 FT DOMAIN 77 108 Framework-3.
 FT DOMAIN 109 115 Complementarity-determining-3.
 FT DISULFID 43 108 By similarity.
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12986 MW; BA852C58F328E1C3 CRC64;

Query Match 78.8%; Score 442; DB 1; Length 115;
 Best Local Similarity 87.4%; Pred. No. 4.4e-38;
 Matches 83; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQDINSYLSWFQKRGKAPKTLIYRANRLVDGVPS 60
 DB 21 DIOMTQSPSSLSASVGDRTVITTCASQDINSYLSWFQKRGKAPKTLIYRANRLVDGVPS 60
 QY 61 RFSGSGSGDYTLTISLQPEDPATYTCQYDEFPYTFGSGTKVEIK 107
 DB 61 RFSGSGSGDYTLTISLQPEDPATYTCQYDEFPYTFGSGTKVEIK 107

RESULT 12

KVIR_HUMAN

AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76023758; PubMed=809329;
 RA Palm W., Hilschmann N.;

ID KVIR_HUMAN STANDARD; PRT; 108 AA.

AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

KA MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose
 RT in Klebsiella polysaccharides K30 and K33."
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -I- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
 CC against 3,4-pyruvylated galactose and isolated from a patient with
 CC Waldenstrom's macroglobulinemia.
 DR PIR; A01876; KIHWE.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C.electrolytic; NAS.
 DR GO; GO:0003823; P.antigen binding; NAS.
 DR GO; GO:0006953; P.immune response; NAS.
 DR InterPro; IPR007110; Ig-1-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.

KW Direct protein sequencing; Immunoglobulin V region;
 KW Monoclonal antibody.

FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

Query Match 78.6%; Score 441; DB 1; Length 108;
 Best Local Similarity 78.5%; Pred. No. 5.2e-38;
 Matches 84; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITTCASQDINSYLSWFQKRGKAPKTLIYRANRLVDGVPS 60
 DB 1 DIOMTQSPSSLSASVGDRTVITTCASQDINSYLSWFQKRGKAPKTLIYRANRLVDGVPS 60
 QY 61 RFSGSGSGDYTLTISLQPEDPATYTCQYDEFPYTFGSGTKVEIK 107
 DB 61 RFSGSGSGDYTLTISLQPEDPATYTCQYDEFPYTFGSGTKVEIK 107

RESULT 13

KVIO_HUMAN

ID KVIO_HUMAN STANDARD; PRT; 108 AA.

AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region Rel.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RT "The primary structure of a crystalline monoclonal immunoglobulin
kappa-type L-chain, subgroup I (Bence-Jones protein Rel): isolation
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
three-dimensional structure of antibodies, in particular the
combinational site." [2]
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).
RN
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.B., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein RFI refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952 (1975).
CC
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1AR2; X-ray; A/B=1-107.
DR PDB; 1BMW; X-ray; A/B=1-107.
DR PDB; 1REI; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
KM Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 36
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 55 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON TER 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E118BCE2A CRC64;

Query Match 78.3%; Score 439; DB 1; Length 108;
Best Local Similarity 79.2%; Pred. No. 8.4e-36;
Matches 84; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Dy 1 DIQMTGSPSSLSASVGDRTVITTCASQDINSYSMPQOKPGKPKTLIYRANRLVDGVP 60
1 DIQMTGSPSSLSASVGDRTVITTCASQDINSYSMPQOKPGKPKTLIYRANRLVDGVP 60
Qy 61 RFGSGSGGDYTLTISLQPEDPATYVCLOYDEFPYFGGCTKVEI 106
61 RFGSGSGGDYTLTISLQPEDPATYVCLOYDEFPYFGGCTKVEI 106
Db 61 RFGSGSGGDYTLTISLQPEDPATYVCLOYDEFPYFGGCTKVEI 106

RESULT 14
ID 06GMX9 PRELIMINARY; PRT; 236 AA.
AC 06GMX9
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueter K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helen F.,
RA Datichenlo L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AA73763.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF77 CRC64;

Query Match 77.9%; Score 437; DB 2; Length 236;
Best Local Similarity 76.6%; Pred. No. 3.4e-37;
Matches 82; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Dy 23 DIQMTGSPSSLSASVGDRTVITTCASQDINSYSMPQOKPGKPKTLIYRANRLVDGVP 60
23 DIQMTGSPSSLSASVGDRTVITTCASQDINSYSMPQOKPGKPKTLIYRANRLVDGVP 60
Qy 61 RFGSGSGGDYTLTISLQPEDPATYVCLOYDEFPYFGGCTKVEI 107
61 RFGSGSGGDYTLTISLQPEDPATYVCLOYDEFPYFGGCTKVEI 107
Db 83 RFGSGSGGDYTLTISLQPEDPATYVCLOYDEFPYFGGCTKVEI 129

RESULT 15
096SA9

```

ID      Q96SA9      PRELIMINARY;      PRT;      107 AA.
AC      Q96SA9;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE      variable region (Fragment).
OS      Homo sapiens (Human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98375893; PubMed=9712075;
RA      Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT      "Molecular analysis of polyclonal monoclonal antibodies from
RT      rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
RT      antibody V region genes."
RL      J. Immunol. 161:2020-2031(1998).
DR      EMBL; U96396; AAB68785.1; -.
DR      PIR; B49047; B49047.
DR      PIR; PH0867; PH0867.
DR      PIR; S16840; S16840.
DR      PIR; S31977; S31977.
DR      PIR; S34083; S34083.
DR      HSSP; P01607; 1BWM.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; Ig, 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
FT      NON_TER      1
FT      NON_TER      1
SQ      SEQUENCE      107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match      77.8%; Score 436.5; DB 2; Length 107;
Best Local Similarity 81.3%; Pred. No. 1.5e-37;
Matches 87; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

QY      1 DIQWTQSPSSLSASVGRVITTCASQDINSYLSMPQKPKAKPKTLTYANRLVDGVPS 60
DB      1 DIQWTQSPSSLSASVGRVITTCASQDINSYLSMPQKPKAKPKTLTYANRLVDGVPS 60
QY      61 RFGSGSGGQDYTLTISLSQPEDPATYVCQYDEFPYTFGGGTVEIK 107
DB      61 RFGSGSGGQDYTLTISLSQPEDPATYVCQYDEFPYTFGGGTVEIK 107
QY      61 RFGSGSGGTDFTLTISLSQPEDPATYVCQYDEFPYTFGGGTVEIK 106
DB      61 RFGSGSGGTDFTLTISLSQPEDPATYVCQYDEFPYTFGGGTVEIK 106

```

Search completed: December 29, 2004, 18:05:21
 Job time : 73.8584 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 16.323 Seconds

(without alignments)
701,451 Million cell updates/sec

Title: US-10-774-076-12

Perfect score: 642

Sequence: 1 EVGLVSGAEVKKRPGASVKI.....GNFPYRDMVGQTLTVSS 119

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:.*
2: PIR1:.*
3: PIR2:.*
4: PIR3:.*
5: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467.5	72.8	137	2 H32513	Ig heavy chain pre
2	459.5	71.6	118	2 S36265	Ig heavy chain V r
3	459.5	71.6	119	2 F30502	Ig heavy chain V r
4	457.5	71.3	128	2 PH0952	Ig heavy chain V r
5	456.5	71.1	150	2 PH0444	Ig heavy chain V r
6	450	70.1	142	2 A32483	Ig heavy chain V r
7	448.5	69.9	120	2 PH0962	Ig heavy chain V r
8	448.5	69.9	128	2 I37267	Ig heavy chain V r
9	448.5	69.9	139	2 A27609	Ig heavy chain pre
10	446.5	69.5	128	2 C37267	Ig heavy chain V r
11	446	69.5	133	2 D33548	Ig heavy chain V-1
12	445.5	69.4	118	2 S38717	Ig heavy chain V r
13	445	69.3	119	2 S20640	Ig heavy chain V r
14	443.5	69.1	116	2 PH0959	Ig heavy chain V r
15	443	69.0	117	2 S03305	Ig heavy chain V r
16	443	69.0	121	2 H37266	Ig heavy chain V r
17	442.5	68.9	124	2 S19665	Ig heavy chain V r
18	442.5	68.9	135	2 S49530	Ig heavy chain V r
19	441.5	68.8	117	2 S25176	Ig heavy chain V r
20	440	68.5	121	2 F32766	Ig heavy chain V r
21	439	68.4	118	2 PL0200	anti-DNA autoantib
22	439	68.4	122	2 S36271	Ig heavy chain V r
23	438.5	68.3	120	2 S41394	Ig heavy chain V r
24	438	68.2	118	2 S38565	Ig heavy chain V r
25	438	68.2	119	2 PH0961	Ig heavy chain V r
26	437.5	68.1	120	2 B22769	Ig heavy chain V r
27	437	68.1	125	2 PH0957	Ig heavy chain V r
28	436	67.9	129	2 S46393	Ig heavy chain V-1
29	436	67.9	133	2 C33548	Ig heavy chain V-1

30	436	67.9	627	2 S14683	Ig mu chain precu
31	435.5	67.8	131	2 S6537	Ig heavy chain V r
32	435.5	67.8	132	2 PH0954	Ig heavy chain V r
33	435	67.8	127	2 PH0955	Ig heavy chain V r
34	435	67.8	129	2 S36260	Ig heavy chain V r
35	435	67.8	129	2 A33548	Ig heavy chain V-1
36	434.5	67.7	116	2 S53751	antibody Fab Jel 1
37	434.5	67.7	122	2 PH0958	Ig heavy chain V r
38	433.5	67.5	126	2 S31600	Ig heavy chain V r
39	433.5	67.5	119	2 MEMS18	Ig heavy chain pre
40	433.5	67.5	287	4 PC4402	peib leader/Ig hea
41	432.5	67.4	126	2 B33548	Ig heavy chain V-1
42	432.5	67.4	138	2 A37267	Ig heavy chain V r
43	432.5	67.4	171	2 S23623	Ig heavy chain V r
44	431	67.1	127	2 S34014	Ig heavy chain V r
45	431	67.1	160	2 PL0105	anti-PR2 erythrocy

ALIGNMENTS

RESULT 1

H32513

Ig heavy chain precursor V region (BXW16) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C:Accession: H32513

R:Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.,

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization and

A:Reference number: A94689; PMID:88313394; PMID:3138286

A:Accession: H32513

A:Molecule type: DNA

A:Residues: 1-137 <KOF>

A:Cross-references: GB:M20831; NID:g196949; PIDN:AA38848.1; PID:g196950

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match	72.8%	Score 467.5;	DB 2;	Length 137;
Best Local Similarity	73.9%;	Pred. No. 8.3e-35;		
Matches	88;	Conservative 14;	Mismatches 16;	Indels 1;
Gaps	1;			
Qy	1	EVGLVSGAEVKKRPGASVKISCVSGYAFPTNMYVRQAPEGLEWIGYIDYGPGRY 60		
Db	20	EIQLQSGAEVLPKASVKSAGSFGYMMWVKOSHGLMIGINIFYGSTSY 79		
Qy	61	SOPEKQATLVYKSTAYMETSLRSEDTAVYYCARGNPFYRDMVGQTLTVSS 119		
Db	80	NQPKKATLVDSSTAYMQLNLTSEDSAVYYCARR-NYSSFDYMGQTLTVSS 137		

RESULT 2

S36265

Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C:Accession: S36265

R:Griffiths, A.D.; Malinvalat, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,

EMBO J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries

A:Reference number: S36256; PMID:93178448; PMID:7679990

A:Accession: S36265

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-118 <GR1>

A:Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	71.6%	Score 459.5;	DB 2;	Length 118;
Best Local Similarity	73.9%;	Pred. No. 3.7e-34;		

Matches

88; Conservative

11; Mismatches

19; Indels

1; Gaps

1;

Qy

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

RESULT 3

F30502

Ig heavy chain V region (A52) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000

C/Accession: F30502

R/Title: D.; Webster, D.M.; Rees, A.R.

A/Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice

A/Reference number: A30502; MUID:88315787; PMID:2457627

A/Accession: F30502

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-119 <Sig>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

F/15-98/Domain: immunoglobulin homology <IMM>

F/15-98/Region: complementarity-determining 3

Query Match

Best Local Similarity

71.3%; Score 457.5; DB 2; Length 128;

Matches 87; Conservative 15; Mismatches 17; Indels 9; Gaps 1;

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

Query Match

Best Local Similarity

71.3%; Score 457.5; DB 2; Length 128;

Matches 87; Conservative 15; Mismatches 17; Indels 9; Gaps 1;

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

Query Match

Best Local Similarity

71.3%; Score 457.5; DB 2; Length 128;

Matches 87; Conservative 15; Mismatches 17; Indels 9; Gaps 1;

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

Db 11 QVOLVSGAEVKKPGASVKISCKVSGYAFITNNYMWYRQAPGKLEWIGITIDPYGDPGY 70
QY 61 SQRKGRATLTVDKSTSTAVNELSLRSEDTAVYYCARRGFPYF-----DYKGG 112
Db 71 AQRKGAVTMRDSTSTAVNELSLRSEDTAVYYCARREKLATTIFGLIITGMDYGG 130
QY 113 TLVTSS 119
Db 131 TLVTSS 137

RESULT 7
PH0962
Ig heavy chain V region (G6+ T-L42) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C/Accession: PH0962
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A/Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0962; MUID:92202880; PMID:1552291
A/Accession: PH0962
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-120 <MAR>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-50/Region: complementarity-determining 2
F/51-67/Region: complementarity-determining 3
F/68-98/Region: framework 3
F/99-108/Region: complementarity-determining 3

Query Match 69.9%; Score 448.5; DB 2; Length 120;
Best Local Similarity 71.9%; Pred. No. 3.6e-33;
Matches 87; Conservative 15; Mismatches 16; Indels 3; Gaps 2;

QY 1 EVOLVSGAEVKKPGASVKISCKVSGYAFITNNYMWYRQAPGKLEWIGITIDPYGDPGY 60
Db 1 QVOLVSGAEVKKPGASVKISCKVSGYAFITNNYMWYRQAPGKLEWIGITIDPYGDPGY 60
QY 61 SQRKGRATLTVDKSTSTAVNELSLRSEDTAVYYCARRG--NEPYFDYGGTTLVTS 118
Db 61 AQRKGAVTMRDSTSTAVNELSLRSEDTAVYYCARGVGRP-HFDYGGTTLVTS 119
QY 119 S 119
Db 120 S 120

RESULT 8
137267
Ig heavy chain V region (129) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C/Accession: 137267
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A/Title: Heavy and light chain variable region sequences and antibody properties of anti-
A/Reference number: A38740; MUID:91177923; PMID:1706720
A/Accession: 137267
A/Status: preliminary; not compared with conceptual translation
A/Residues: 1-128 <RUF>
A/Molecule type: mRNA
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/19-102/Domain: immunoglobulin homology <IMM>

Query Match 69.9%; Score 448.5; DB 2; Length 128;
Best Local Similarity 71.5%; Pred. No. 3.8e-33;
Matches 88; Conservative 9; Mismatches 21; Indels 5; Gaps 1;

QY 2 VOLVSGAEVKKPGASVKISCKVSGYAFITNNYMWYRQAPGKLEWIGITIDPYGDPGY 61
Db 6 VOLVSGAEVKKPGASVKISCKVSGYAFITNNYMWYRQAPGKLEWIGITIDPYGDPGY 65
QY 62 QRKGRATLTVDKSTSTAVNELSLRSEDTAVYYCARRG-----NEPYFDYGGTTLV 116
Db 66 QRKGRATLTVDKSSSTAVNELSLRSEDTAVYYCARRGITLVVAKSYFDYGGTTLV 125
QY 117 VSS 119
Db 126 VSS 128

RESULT 9
A27609
Ig heavy chain precursor V region (129) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C/Accession: A27609
R/Klein, D.; Metcupaki, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A/Title: 1.29 lymphoma cells express a nonmutated V-H gene before and after H chain swi
A/Reference number: A27609; MUID:88154467; PMID:3126234
A/Accession: A27609
A/Molecule type: DNA
A/Residues: 1-139 <KLR>
A/Cross-references: EMBL:M19401; NID:G195441; PIDN:AAA38303.1; PID:G553992
C/Genetics: 16/1
A/Intons: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-139/Product: Ig heavy chain V region 129 #status predicted <VAR>
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.9%; Score 448.5; DB 2; Length 139;
Best Local Similarity 71.7%; Pred. No. 4.2e-33;
Matches 86; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

QY 1 EVOLVSGAEVKKPGASVKISCKVSGYAFITNNYMWYRQAPGKLEWIGITIDPYGDPGY 60
Db 20 EVOLVSGAEVKKPGASVKISCKVSGYAFITNNYMWYRQAPGKLEWIGITIDPYGDPGY 79
QY 61 SQRKGRATLTVDKSTSTAVNELSLRSEDTAVYYCARRGFPYF--FDYGGTTLVTS 119
Db 80 NQRKGRATLTVDKSSSTAVNELSLRSEDTAVYYCARVSYSDYMDYGGTTLVTS 139

RESULT 10
C37267
Ig heavy chain V region (Py69) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C/Accession: C37267
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A/Title: Heavy and light chain variable region sequences and antibody properties of ant
A/Reference number: A38740; MUID:91177923; PMID:1706720
A/Accession: C37267
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-128 <RUF>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/19-102/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 446.5; DB 2; Length 128;
Best Local Similarity 69.9%; Pred. No. 5.8e-33;
Matches 86; Conservative 11; Mismatches 21; Indels 5; Gaps 1;

QY 2 VOLVSGAEVKKPGASVKISCKVSGYAFITNNYMWYRQAPGKLEWIGITIDPYGDPGY 61
Db 2 VOLVSGAEVKKPGASVKISCKVSGYAFITNNYMWYRQAPGKLEWIGITIDPYGDPGY 61

Dh 6 VOLQSGAEVKKPGASVKISKCTGTYFTETHTHWKQSGKLEWIGRFPNPGSGSTYN 65
Qy 62 OKFKGKATLTVDKSTSTAYMELSLRSEDPAVYTCARGNF-----PYFDYWGQGLTVT 116
Db 66 OKFKGKATLTVDKSSSTAYMELSLRSEDPAVYTCARGNFYGYTYTFDYWGQGLTVT 125
Qy 117 VSS 119
Db 126 VSS 128

RESULT 11

D33548
Ig heavy chain V-1 region (MIL2) - human
C/Species: Homo sapiens (man)
C/Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #ext_change 16-Aug-1996
C/Accession: D33548
R/Klpp, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A/Title: Developmentally restricted immunoglobulin heavy chain variable region expr
A/Reference number: A33548; MUID:89345575; PMID:2503826
A/Accession: D33548
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A/Molecule type: mRNA
A/Residues: 1-123 <KIP>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 446; DB 2; Length 123;
Best Local Similarity 67.5%; Pred. No. 6.2e-33;
Matches 83; Conservative 18; Mismatches 18; Indels 4; Gaps 1;

Qy 1 EVOLVSGAEVKKPGASVKISKVGYAFNTNMYWVROAPGKLEWIGTIDPYGDPGY 60
Db 1 QVOLVSGAEVKKPGASVKISCEASGYFTGHVHWKQAPGQGLEWGMINPNSGGTNY 60
Qy 61 SOKFKGKATLTVDKSTSTAYMELSLRSEDPAVYTCARGNF---NPFYFDYWGQGLTVT 116
Db 61 AKKQGRVITTRDTSINTAYMELSLRSDPAVYTCARASYCYGVDYFPDYWGQGLTVT 120
Qy 117 VSS 119
Db 121 VSS 123

RESULT 12

S38717
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C/Accession: S38717
R/Cimatis, A.Y.
submitted to the EMBL Data Library, November 1993
A/Reference number: S38713
A/Accession: S38717
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-118 <CIM>
A/Cross-references: EMBL:X65020; NID:g416099; PIDN:CAA53607.1; PID:g1334262
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.4%; Score 445.5; DB 2; Length 118;
Best Local Similarity 72.9%; Pred. No. 6.5e-33;
Matches 86; Conservative 11; Mismatches 18; Indels 3; Gaps 2;

Qy 3 QVOLVSGAEVKKPGASVKISKVGYAFNTNMYWVROAPGKLEWIGTIDPYGDPGY 62
Db 3 QVOLVSGAEVKKPGASVKISKVGYAFNTNMYWVROAPGKLEWIGTIDPYGDPGY 62
Qy 63 KKKGKATLTVDKSTSTAYMELSLRSEDPAVYTCAR--GNPFYFDYWGQGLTVTSS 119

Db 63 KFKGKATLTVDKSTSTAYMELSLRSEDPAVYTCARGNF---YFDYWGQGLTVTSS 118

RESULT 13

S20640
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 23-Jul-1999
C/Accession: S20640; S20644
R/Josman, M.; Faas, T.W.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A/Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A/Reference number: S20639
A/Accession: S20640
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-119 <LOS>
A/Cross-references: EMBL:X65002; NID:g52600; PIDN:CAA46135.1; PID:g52601; EMBL:X64999; ;
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.3%; Score 445; DB 2; Length 119;
Best Local Similarity 70.6%; Pred. No. 7.3e-33;
Matches 84; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EVOLVSGAEVKKPGASVKISKVGYAFNTNMYWVROAPGKLEWIGTIDPYGDPGY 60
Db 1 EVOLVSGAEVKKPGASVKISKVGYAFNTNMYWVROAPGKLEWIGTIDPYGDPGY 60
Qy 61 SOKFKGKATLTVDKSTSTAYMELSLRSEDPAVYTCARGNF---NPFYFDYWGQGLTVTSS 119
Db 61 NEMFKGKATLTVDKSSSTAYMELSLRSEDPAVYTCARATKSGWPAFYWGQGLTVTSSA 119

RESULT 14

PH0959
Ig heavy chain V region (G6+ T-126) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C/Accession: PH0959
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Klpp, T.J.
J. Exp. Med. 175, 983-991, 1992
A/Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0952; MUID:92202880; PMID:1552291
A/Accession: PH0959
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-116 <MAR>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>
F/15-98/Region: framework 1
F/31-35/Region: complementarity-determining 1
F/36-50/Region: complementarity-determining 2
F/51-67/Region: complementarity-determining 3
F/68-98/Region: framework 3
F/99-104/Region: complementarity-determining 3

Query Match 69.1%; Score 443.5; DB 2; Length 116;
Best Local Similarity 71.4%; Pred. No. 9.7e-33;
Matches 85; Conservative 15; Mismatches 16; Indels 3; Gaps 1;

Qy 1 EVOLVSGAEVKKPGASVKISKVGYAFNTNMYWVROAPGKLEWIGTIDPYGDPGY 60
Db 1 QVOLVSGAEVKKPGASVKISKVGYAFNTNMYWVROAPGQGLEWGIIPRTGANY 60
Qy 61 SOKFKGKATLTVDKSTSTAYMELSLRSEDPAVYTCARGNF---NPFYFDYWGQGLTVTSS 119
Db 61 AKKQGRVITTRDTSINTAYMELSLRSEDPAVYTCARGN---WFDYWGQGLTVTSS 116

Mon Jan 3 13:38:48 2005

```

RESULT 15
S03305
Ig heavy chain V region (6B12) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C/Accession: J10044; S05276; S03305
R/Van Cleave, V.H.; Naeve, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A/Title: Do antibodies recognize amino acid side chains of protein antigens independent?
A/Reference number: J10043; MUID:86258372; PMID:2455014
A/Accession: J10044
A/Molecule type: mRNA
A/Residues: 1-117 <VAN>
A/Cross-references: EMBL:X12381
R/Metzger, D.W.
submitted to the EMBL Data Library, July 1988
A/Reference number: S05276
A/Accession: S05276
A/Molecule type: mRNA
A/Residues: 1-116, 'T' <MET>
A/Cross-references: EMBL:X12381, NID:952094; PIDN:CA30939.1; PID:9930170
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 443; DB 2; Length 117;
Best Local Similarity 72.3%; Pred. No. 1,1e-32;
Matches 86; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVQLVDSGAEVKKPKASVKISCKVGYAFITNYMMWVWQAQPGKLEWIGYIDPYGDPGY 60
DB 1 EVQLVDSGAEVKKPKASVKISCKVGYAFITNYMMWVWQAQPGKLEWIGYIDPYGDPGY 60
QY 61 SQRKKGATLTVDKSTSTAYMELSSLRSEDTAVYVCARGNFPYFDYWGQGLVTVSS 119
DB 61 SQRKKGATLTVDKSTSTAYMELSSLRSEDTAVYVCARGNFPYFDYWGQGLVTVSS 119

```

Search completed: December 29, 2004, 18:06:58
 Job time : 17.4897 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:38:43 ; Search time 82.1416 Seconds

(without alignments)
833.556 Million cell updates/sec

Title: US-10-774-076-12

Perfect score: 642
Sequence: 1 EVOLVQSGAEVKKKPGASVKI.....GNPFYDPYWGQGLTVTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_02.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	72.9	120	Q920E8	Q920E8 mus musculu
2	454	70.7	119	Q9UL94	Q9UL94 mus musculu
3	450.5	70.2	124	Q9UL92	Q9UL92 mus musculu
4	449	69.9	464	AAH19337	AAH19337 mus sapien
5	448.5	69.9	498	Q6N041	Q6N041 mus sapien
6	448.5	69.9	498	CAE45829	CAE45829 mus sapien
7	445	69.3	123	Q8V1J1	Q8V1J1 mus musculu
8	445	69.3	146	Q924R8	Q924R8 mus musculu
9	441.5	68.8	465	Q6PUB2	Q6PUB2 mus musculu
10	441.5	68.8	465	AAH18280	AAH18280 mus musculu
11	440	68.5	470	Q7TMM1	Q7TMM1 mus musculu
12	439	68.4	119	Q9GYZ2	Q9GYZ2 schistosoma
13	439	68.4	472	Q6PJA7	Q6PJA7 mus musculu
14	439	68.4	472	AAH18535	AAH18535 mus muscu
15	438	68.2	117	Q9QXFO	Q9QXFO mus musculu
16	438	68.2	470	AAH62336	AAH62336 mus sapien
17	433.5	67.5	139	AAH07 MOUSE	AAH07 MOUSE
18	433.5	67.5	145	Q924Q7	Q924Q7 mus musculu
19	433	67.4	144	Q924P5	Q924P5 mus musculu
20	432.5	67.4	145	Q924R4	Q924R4 mus musculu
21	431.5	67.2	467	AAH37361	AAH37361 mus sapien
22	430.5	67.1	145	Q924Q6	Q924Q6 mus musculu
23	430.5	67.1	145	Q924R1	Q924R1 mus musculu
24	430.5	67.1	159	Q96080	Q96080 mus sapien
25	429.5	66.9	145	Q924Q9	Q924Q9 mus musculu
26	429.5	66.9	482	Q8K172	Q8K172 mus musculu
27	429	66.8	473	Q9DBL4	Q9DBL4 mus musculu
28	428.5	66.7	116	Q9UL89	Q9UL89 mus sapien
29	428.5	66.7	145	Q924P7	Q924P7 mus musculu
30	428	66.7	117	HV12 MOUSE	HV12 MOUSE
31	426.5	66.4	143	Q924R0	Q924R0 mus musculu

32	426.5	66.4	143	Q924R7	Q924R7 mus musculu
33	426.5	66.4	145	Q924R3	Q924R3 mus musculu
34	426.5	66.4	481	Q8VCV5	Q8VCV5 mus musculu
35	426.5	66.4	518	Q6N030	Q6N030 mus sapien
36	426.5	66.4	518	CAE45841	CAE45841 mus sapien
37	426	66.4	125	Q9UL95	Q9UL95 mus sapien
38	426	66.4	142	Q924Q1	Q924Q1 mus musculu
39	425	66.2	146	Q924Q3	Q924Q3 mus musculu
40	424.5	66.1	109	Q9UL75	Q9UL75 mus musculu
41	424.5	66.1	473	Q99J25	Q99J25 mus musculu
42	424	66.0	140	Q924R2	Q924R2 mus musculu
43	423.5	66.0	143	Q924Q5	Q924Q5 mus musculu
44	423	65.9	117	Q9QX89	Q9QX89 mus musculu
45	423	65.9	614	Q7TMT6	Q7TMT6 mus musculu

ALIGNMENTS

RESULT 1

ID	Q920E8	PRELIMINARY;	PRT;	120 AA.
AC	Q920E8;			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	Pterin-mimicking anti-idiotope heavy chain variable region (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Actin J.D., Japae A., Jennings I.G., Horaiis O., Cotton R.G.H.;			
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF307936; AL09420.1; -			
DR	HSSP; P01751; INOB.			
DR	InterPro; IPR007110; Ig_1like.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IG_1.			
DR	PROSITE; PSS0835; IG_LIKE; 1.			
FT	NON_TER			
FT	NON_TER			
SQ	SEQUENCE 120 AA; 13204 MW; DC4834ABID56F3C CRC64;			
Query Match 72.9%; Score 468; DB 2; Length 120;				
Best Local Similarity 75.0%; Pred. No. 1.8e-40;				
Matches 90; Conservative 10; Mismatches 18; Indels 2; Gaps 1;				
Qy	1	EVOLVQSGAEVKKKPGASVKISCKVSGYAFNTNNMVRQAPGKLEWIGYIDPYGPGY	60	
Db	1	EVOLVQSGAEVKKKPGASVKISCKVSGYAFNTNNMVRQAPGKLEWIGYIDPYGPGY	60	
Qy	61	SGKPKKATITVDKSTAYAMEISLRSEPTANYTCA--RRGNPFYDPYWGQGLTVTVSS	118	
Db	61	NQKFKKATITVDKSTAYAMEISLRSEPTANYTCA--RRGNPFYDPYWGQGLTVTVSS	120	
RESULT 2				
ID	Q9UL94	PRELIMINARY;	PRT;	119 AA.
AC	Q9UL94;			
DT	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			

RP [1]
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetuses."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01751; INOB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Ig_v.1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1 119
SQ SEQUENCE 119 AA; 13205 MW; 1364F5345F4A16E CRC64;
Query Match 70.7%; Score 454; DB 2; Length 119;
Best Local Similarity 72.3%; Pred. No. 5e-39;
Matches 86; Conservative 12; Mismatches 21; Indels 0; Gaps 0;
QY 1 EVOLVSGAEVKKRPGASVSKVSGYAFNNMNTWVROAPGKGLWIGYIDPYGDPGY 60
DB 1 EVOLVSGAEVKKRPGASVSKVSGYAFNNMNTWVROAPGKGLWIGYIDPYGDPGY 60
QY 61 SQKFKGKATLVVDKSTSTAYMELSLRSEDYAVYCARGNFPYDPYGGGTLTVVSS 119
DB 61 AQKFGKATLVVDKSTSTAYMELSLRSEDYAVYCARGNFPYDPYGGGTLTVVSS 119
RESULT 3
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9827139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetuses."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSSP; P01751; INOB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; Ig_v.1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;
Query Match 70.2%; Score 450.5; DB 2; Length 124;
Best Local Similarity 70.4%; Pred. No. 1.2e-38;
Matches 88; Conservative 13; Mismatches 17; Indels 7; Gaps 2;
QY 1 EVOLVSGAEVKKRPGASVSKVSGYAFNNMNTWVROAPGKGLWIGYIDPYGDPGY 60
DB 1 EVOLVSGAEVKKRPGASVSKVSGYAFNNMNTWVROAPGKGLWIGYIDPYGDPGY 60
QY 61 SQKFKGKATLVVDKSTSTAYMELSLRSEDYAVYCARGNFPYDPYGGGTLTVVSS 114

DB 61 AQKFGKATLVVDKSTSTAYMELSLRSEDYAVYCARGLYVVPAPARSRDYNQGTLL 119
QY 115 VTWSS 119
DB 120 VTWSS 124
RESULT 4
ID AAH19337 PRELIMINARY; PRT; 464 AA.
AC AAH19337;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2338257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madden A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzywinski M.I., Skalska J., Smalish D.E., Schermer A., Schein J.E.,
RA Jones S.J., Morris M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TTSUB=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019337; AAH19337.1; -.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 50891 MW; 2F80673E74E2A85 CRC64;
Query Match 69.9%; Score 449; DB 2; Length 464;
Best Local Similarity 72.3%; Pred. No. 7.7e-28;
Matches 86; Conservative 11; Mismatches 18; Indels 4; Gaps 1;
QY 1 EVOLVSGAEVKKRPGASVSKVSGYAFNNMNTWVROAPGKGLWIGYIDPYGDPGY 60
DB 20 QVQVLSGAEVKKRPGASVSKVSGYAFNNMNTWVROAPGKGLWIGYIDPYGDPGY 79
QY 61 SQKFKGKATLVVDKSTSTAYMELSLRSEDYAVYCARGNFPYDPYGGGTLTVVSS 119
DB 80 AQKFGKATLVVDKSTSTAYMELSLRSEDYAVYCARGLYVVPAPARSRDYNQGTLL 134
RESULT 5
ID Q6N041 PRELIMINARY; PRT; 498 AA.
AC Q6N041;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)


```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067781; BAB63266.1; -.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 146
SQ SEQUENCE 146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;

Query Match 69.3%; Score 445; DB 2; Length 146;
Best Local Similarity 70.2%; Pred. No. 5.3e-38;
Matches 85; Conservative 14; Mismatches 20; Indels 2; Gaps 1;

QY 1 EVQLVDSGAEVKKRQASVKISCKVSGYAFNINMYRWQAPGKLEWIGYIDPYGDPGY 60
DB 1 QVQLQQPAAELVKKPQASVKSCKASGYTFTSYMMHWKQRPQGLEWIGIDNSGDTK 60
QY 61 SQKPKGKATLTVDKSTSTAYMELSLRSEDPAYVYCAR--GNPPYFDYWGQGITLVYS 118
DB 61 NEKFKGKATLTVDKSSSTAYMELSLRSEDPAYVYCAR--GNPPYFDYWGQGITLVYS 120
QY 119 S 119
DB 121 S 121

```

```

RESULT 9
O6PUB2
ID O6PUB2 PRELIMINARY; PRT; 465 AA.
AC O6PUB2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Mnt1 model.

```

```

RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldi M.P., Casavant T.L., Schetz T.E.,
RA Baha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard J.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Mnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018280; AAH18280.1; -.
DR InterPro; IPR003599; Ig_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00654; C1-set; 3.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51329 MW; 394F3C4EB8DB3E21 CRC64;

Query Match 68.8%; Score 441.5; DB 2; Length 465;
Best Local Similarity 70.6%; Pred. No. 4.6e-37;
Matches 84; Conservative 12; Mismatches 20; Indels 3; Gaps 1;

QY 1 EVQLVDSGAEVKKRQASVKISCKVSGYAFNINMYRWQAPGKLEWIGYIDPYGDPGY 60
DB 20 QVQLQQPAAELVKKPQASVKSCKASGYTFTSYMMHWKQRPQGLEWIGYFDYNDTKC 79
QY 61 SQKPKGKATLTVDKSTSTAYMELSLRSEDPAYVYCARGNPPYFDYWGQGITLVYS 119
DB 80 NEKFKGKATLTADKSSSTAYMELSLRSEDPAYVYCAR---YYPFDYWGQGITLVYS 135

```

```

RESULT 10
AAH18280
ID AAH18280 PRELIMINARY; PRT; 465 AA.
AC AAH18280;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor;

```

```

RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Vadim T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abrahamson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC018280; AAH18280.1; -.
KM Hypothetical protein.
SQ SEQUENCE 465 AA; 51329 MW; 394FA3C4EBDB3E21 CRC64;

Query Match 68.8%; Score 441.5; DB 2; Length 465;
Best Local Similarity 70.6%; Pred. No. 4,66-37;
Matches 84; Conservative 12; Mismatches 20; Indels 3; Gaps 1;

QY 1 EVOLVSGAEVKKPGASVKISCKVSGYAFITNNMWRQAPGKLEWIGYIDPYGPGY 60
DB 20 EVOLVSGAEVKKPGASVKISCKVSGYAFITNNMWRQAPGKLEWIGYIDPYGPGY 79
QY 61 SQRKGRATLTVDKSTSTAYMELSLSEDTAVYTCARNGFPYFPYGGTGLVTV 119
DB 80 NEKRGKATLTVDKSTSTAYMELSLSEDTAVYTCARNGFPYFPYGGTGLVTV 135

RESULT 11
Q7TMK1 PRELIMINARY; PRT; 470 AA.
AC Q7TMK1;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein A1324046.
GN Name=A1324046;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Vadim T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abrahamson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

```

```

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RA Expression driven by an MMTV-LTR enhancer.;
RC Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC055910; AAH55910.1; -.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; CI-set; 3.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS00835; IG-LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90B4DF96BB090 CRC64;

Query Match 68.5%; Score 440; DB 2; Length 470;
Best Local Similarity 70.5%; Pred. No. 6,7e-37;
Matches 86; Conservative 13; Mismatches 19; Indels 4; Gaps 2;

QY 1 EVOLVSGAEVKKPGASVKISCKVSGYAFITNNMWRQAPGKLEWIGYIDPYGPGY 60
DB 20 EVOLVSGAEVKKPGASVKISCKVSGYAFITNNMWRQAPGKLEWIGYIDPYGPGY 79
QY 61 SQRKGRATLTVDKSTSTAYMELSLSEDTAVYTCARNGFPYFPYGGTGLVTV 117
DB 80 NEKRGKATLTVDKSTSTAYMELSLSEDTAVYTCARNGFPYFPYGGTGLVTV 138

QY 118 SS 119
DB 139 SS 140

RESULT 12
Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
DE (Fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RC Song X.T., Feng Z.Q., Guan X.H.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR HSBP; AF282622; AAC01452.1; -.
DR HSBP; P01751; 1A6W.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR PROSITE: PS00835; IG-LIKE; 1.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFA6AB CRC64;

```

Query Match 68.4%; Score 439; DB 2; Length 119;
Best Local Similarity 69.7%; Pred. No. 1.8e-37;
Matches 83; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

QY 1 EVOLVQSGAEVKKPGASVKISCKVSGYAFNTNMYWVROAPGKLEWIGYIDPYGDPGY 60
DB 1 QVQLVDSGAEVKKPGASVKISCKVSGYAFNTNMYWVROAPGKLEWIGYIDPYGDPGY 60
QY 61 SOKFKGKATLTVDKSTSTAYMELSLRSBEDTAVYCARPNFPYEDYWGQGLTVT 119
DB 61 NQKFKRATLTVDKSTSTAYMELSLRSBEDTAVYCARPNFPYEDYWGQGLTVT 119

RESULT 13

06PUJ7 PRELIMINARY; PRT; 472 AA.
AC 06PUJ7, 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Wozniy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer;
RX Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018535; AAH18535.1; -
DR InterPro; IPR003599; IG_1ike.
DR InterPro; IPR003597; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-sect; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IgC1; 3.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00230; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.

SO SEQUENCE 472 AA, 52299 MW, 165169C23D55D4AB CRC64;

Query Match 68.4%; Score 439; DB 2; Length 472;
Best Local Similarity 69.1%; Pred. No. 8.5e-37;
Matches 85; Conservative 14; Mismatches 20; Indels 4; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKISCKVSGYAFNTNMYWVROAPGKLEWIGYIDPYGDPGY 60
DB 20 EVQLVDSGAEVKKPGASVKISCKVSGYAFNTNMYWVROAPGKLEWIGYIDPYGDPGY 79
QY 61 SOKFKGKATLTVDKSTSTAYMELSLRSBEDTAVYCARPNFPYEDYWGQGLTVT 116
DB 80 NQKFKRATLTVDKSTSTAYMELSLRSBEDTAVYCARPNFPYEDYWGQGLTVT 139

QY 117 VSS 119

DB 140 VSS 142

RESULT 14

ID AAH18535 PRELIMINARY; PRT; 472 AA.
AC AAH18535;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Wozniy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018535; AAH18535.1; -
KW Hypothetical protein.

Query Match 68.4%; Score 439; DB 2; Length 472;
Best Local Similarity 69.1%; Pred. No. 8.5e-37;
Matches 85; Conservative 14; Mismatches 20; Indels 4; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKISCKVSGYAFNTNMYWVROAPGKLEWIGYIDPYGDPGY 60
DB 20 EVQLVDSGAEVKKPGASVKISCKVSGYAFNTNMYWVROAPGKLEWIGYIDPYGDPGY 79
QY 61 SOKFKGKATLTVDKSTSTAYMELSLRSBEDTAVYCARPNFPYEDYWGQGLTVT 116

Db 80 NQKFKGKATLTVDKSSSTAYWELSLTSEDGAVVYCARGYISYSDHFFDYMGGTTIT 139
QY 117 VSS 119
Db 140 VSS 142

RESULT 15

09QXF0 PRELIMINARY; PRT; 117 AA.
ID 09QXF0
AC 09QXF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ225171; CAB5236.1; -
DR PIR; PH0973; PH0973.
DR HSSP; P01751; INGB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0035; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MM; D816AD0858A47E4C CRC64;

Query Match 68.2%; Score 438; DB 2; Length 117;
Best local similarity 71.4%; Pred. No. 2.2e-37;
Matches 85; Conservative 13; Mismatches 19; Indels 2; Gaps 1;

QY 1 EVQLVQSGAEVKKPGQSVYKISKVGAFTNYMMYVRQAPGKLEWIGYIDPYGDPGY 60
Db 1 EVQLVQSGPELVKPGASVTRKCSKASGYTFDYMKWKVQSHGKSLIEWIGDINPNNGTSY 60
QY 61 SQKFKGKATLTVDKSTSTAYWELSLSEDPAVYTCARGNFPYTFDYMGGTTLTVSS 119
Db 61 NQKFKGKATLTVDKSSSTAYWELSLSEDGAVVYCAR--DKDYFFDYMGGTTLTVSS 117

Search completed: December 29, 2004, 18:05:21
Job time : 83.1416 secs

THIS PAGE BLANK (USE)

XX This is the amino acid sequence of the heavy chain variable region (VH)
CC of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody
CC D14H2HC 1-0. It is based on the VH sequence (see AAW84095) of human Kabat
CC subgroup I VH, with complementarity determining regions (CDRs) from the
CC murine anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC D12 (see AAW84093). 7 Murine framework residues (24, 48, 67, 68, 70, 72
CC and 74) are retained. The humanised heavy chain can be expressed in host
CC cells using nucleic acid molecules (see AAW17299) of the invention.
CC Humanised D12 VH is also provided (see AAW84096). The humanised
CC antibodies can be used for passive immunotherapy of disorders mediated by
CC the alpha-v beta-3 receptor, e.g. cardiovascular or angiogenic-related
CC disorders, such as angiogenesis and restenosis associated with diabetic retinopathy,
CC atherosclerosis and restenosis, chronic inflammatory disorders, macular
CC degeneration, rheumatoid arthritis and cancer, e.g. solid tumour
CC metastasis, and diseases where bone resorption is associated with
CC pathology such as osteoporosis, hyperparathyroidism, Paget's disease,
CC hypercalcaemia of malignancy, osteolytic lesions produced by bone
CC metastasis, bone loss due to immobilisation or sex hormone deficiency.
CC They can also be used for targeted drug therapy, and for detection and
CC diagnosis

Sequence 117 AA;

Query Match	82.6%;	Score 530;	DB 2;	length 117;
Best Local Similarity	85.1%;	Pred. No. 7.7e-39;		
Matches 103;	Conservative 7;	Mismatches 5;	Indels 6;	Gaps 2
QY	1	EVQLVDSGAEVKKPKASVYKISCKVSGVGFPTNNMYWTRQA	PGKGLEIGITDPYGDPEY	60
	:			
Db	1	QVQLVDSGAEVKKPKASVYKISCKVSGVGFPTNNMYWTRQA	PGKGLEIGITDPYGDPEY	60
	:			
QY	61	SOKEFGKATLLVDSKSTAVNMLSLRSEDPAVYVCARR--GNPYYFDYMGQGLTVTVS		118
	:			
Db	61	NQKFGKATLLVDSKSTAVNMLSLRSEDPAVYVCARR--GNPYYFDYMGQGLTVTVS		116
	:			
QY	119	S	119	
	:			
Db	117	S	117	
	:			

RESULT 2
ID AAW71880
AAW71880 standard; protein; 588 AA.
AC AAW71880;
DT 18-JAN-1999 (first entry)
IDB Anti-human Fas humanised antibody CH11 heavy chain hmuh.
XX Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis; autoimmune disease; rheumatoid arthritis; therapy; human; antibody engineering.
OS Homo sapiens. Synthetic.
Key Location/Qualifiers Peptide 1..19 Protein /label= Sig_peptide 20..588 Region /label= Mat_protein 50..54 /label= CDR1 /note= "complementarity determining region 1 from CH11 heavy chain" 69..84 /label= CDR2 heavy chain heavy chain 118..124 /label= CDR3
Region
Region

FT		/note= "complementarity determining region 3 from CH11
FT		heavy chain"
XX		
XX		
PN	EP866131-A2.	
XX		
XX		
PD	23-SEP-1998.	
XX		
PF	20-MAR-1998;	98EP-00302113.
XX		
PR	21-MAR-1997;	97JP-00067938.
XX		
XX		
PA	(SANY) SANKYO CO LTD.	
XX		
PI	Seizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;	
XX		
DR	WPI; 1998-482965/42.	
XX	N-FSDb; AAV61363.	
XX		
PT	Production of anti-Fas protein humanised antibodies - for use in inducing	
PT	apoptosis on Fas expressing cells in the treatment of auto-immune	
PT	diseases, especially rheumatoid arthritis.	
XX		
PS	Claim 21; Page 105-107; 187pp; English.	
XX		

CC This is the amino acid sequence of a humanised anti-Fas antibody CH11
CC heavy chain, designated HmH. HmH is based on the heavy chain (see
CC AA071868) of murine anti-human Fas monoclonal antibody CH11. The
CC humanised sequence was designed following selection of donor residues
CC from CH11 to be grafted onto acceptor molecule 21.26/CL. 2 Heavy chain
CC sequences (see AA071860-81) have been designed, and each can be used in
CC combination with any of 4 light chain sequences (see AA071876-79) to
CC provide novel, claimed humanised CH11 IgM antibodies that lack a J chain.
CC These humanised anti-human Fas antibodies are capable of inducing
CC apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in
CC the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA
CC sequences encoding the humanised antibodies are claimed, as are vectors
CC such as pHRM5-1 including the HmH nucleotide sequence (see AA061363),
CC and host cells such as Escherichia coli pHRM5-1 (FERM BP-5863)
XX
XX
Sequence 588 AA;

	Query Match	78.6%	Score 504.5;	DB 2,	Length 588;	
	Best Local Similarity	81.7%	Pred. No. 6.6e-36;			
	Matches	98;	Conservative	6;	Mismatches 11,	Indels 5, Gaps 2
QY	1 EYVLVSGAEVKKPKPASVYKISCVXSVGAFTNNMYWVRQAAPGKGLWMIGYIDPYGGDPGY	60				
Dd	20 EYVLVSGAEVKKPKPASVYKVSCKASGYTFPDYNMHWVRQAAPGGLEMGVIYPNNGTGY	79				
QY	61 SOKFKGKATLTVADKSTAYVMELSLISEPTAVYYCARAGNPFFYY-FDYWGCGTLVTWSS	119				
Dd	80 NQKFPSKATLTVDNASASTAYVMELSSLISEPTAVYYCAR-----SYAMDYWGGLVTWSS	135				
 RESULT 3						
ID	AAB12917					
XX	AAB12917 standard; protein; 588 AA.					
XX	AAB12917;					
DT	16-NOV-2000 (first entry)					
DE	Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #86.					
XX	KW Anti-rheumatic agent; immunoglobulin M; IgM; apoptosis inducer;					
XX	KW immunosuppression; autoimmune disease; treatment; rheumatism;					
XX	anti-Fas antibody.					
OS	Synthetic.					
JF	JP2000154149-A.					
06-JUN-2000.						

XX 17-SEP-1999; 99JP-00263984.
XX 18-SEP-1998; 98JP-00264598.
XX (SANY) SANKYO CO LTD.
XX WPI; 2000-454476/40.
XX N-PSDB; AAA78271.
XX Anti-human Fas humanizing antibody-containing antirheumatic agents.
XX Claim 1; Page 75-77; 109pp; Japanese.
XX The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially rheumatism. The IgM molecule used in the invention has human Fas-antigen binding properties. Included in the invention are nucleotide sequences of the IgM light and heavy chains (see AAA78267-A78272) and the corresponding protein sequences (see AAA782913-B12918 and AAB12919), and CC nucleotide sequences of the humanised anti-human Fas Ig CH1 (see CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). A180 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907). CC Primers specific for the anti-human Fas antibody, light, heavy and kappa CC chains used in the invention are represented by sequences AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the CC invention are represented by sequences AAA78277-A78318 and AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are CC represented by sequences AAA78321-A78334 and AAA78336-A78367. Primer CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in CC the production of the agent of the invention
XX
XX Sequence 588 AA;
SQ
Query Match 78.6%; Score 504.5; DB 3; Length 588;
Best Local Similarity 81.7%; Pred. No. 6.6e-36;
Matches 98; Conservative 6; Mismatches 11; Indels 5; Gaps 2;
QY 1 EVOLVSGAEVKKPGASVKISCKVSGYAFNINMYWROAPGKLEWIGYIDPYGPGY 60
DB 20 EVOLVSGAEVKKPGASVKISCKVSGYAFNINMYWROAPGKLEWIGYIDPYGPGY 79
QY 61 SQFKGKATLVTKSTSTAVMELSLRSEPTAVYYCARRGFPYY-PDYMGQGLTVTVSS 119
DB 80 NQFKSKATLVTKSTSTAVMELSLRSEPTAVYYCAR---SYANDYMGQGLTVTVSS 135
RESULT 4
ADL1892
ID ADL1892 standard; peptide; 117 AA.
AC ADL1892;
XX
XX 06-MAY-2004 (first entry)
XX CDR transplant antibody heavy chain variable region #3.
XX cancer metastasis; human vascular endothelial growth factor; VEGF;
XX receptor Flt-1; Cytostatic; lung cancer; CDR.
XX Homo sapiens.
XX OS
XX JP2003261460-A.
XX 16-SEP-2003.
XX 08-MAR-2002; 2002JP-00063835.
XX 08-MAR-2002; 2002JP-00063835.
XX

XX (KYOW) KYOWA HAKKO KOGYO KK.
XX (SHIB/) SHIBUYA T.
XX WPI; 2004-056096/06.
XX Preventive or therapeutic agent of lung selective cancer metastasis
XX containing the substance which inhibits the information transmission
XX PT which intervenes human VEGF receptor Flt-1 as an active ingredient.
XX Claim 18; SEQ ID NO 19; 36pp; Japanese.
XX
XX The present invention relates to a preventive or therapeutic agent of CC lung selective cancer metastasis containing the substance which inhibits CC the information transmission which intervenes human vascular endothelial CC growth factor (VEGF) receptor Flt-1 as an active ingredient. The CC invention is useful for inhibiting spread of lung cancer, and effectively CC controls the spread of lung cancer. The present sequence represents a CDR CC transplant antibody heavy chain variable region.
XX
XX Sequence 117 AA;
SQ
Query Match 78.5%; Score 504; DB 8; Length 117;
Best Local Similarity 80.7%; Pred. No. 1.5e-36;
Matches 96; Conservative 9; Mismatches 12; Indels 2; Gaps 1;
QY 1 EVOLVSGAEVKKPGASVKISCKVSGYAFNINMYWROAPGKLEWIGYIDPYGPGY 60
DB 1 QVOLVSGAEVKKPGASVKISCKVSGYAFNINMYWROAPGKLEWIGYIDPYGPGY 60
QY 61 SQFKGKATLVTKSTSTAVMELSLRSEPTAVYYCARRGFPYY-PDYMGQGLTVTVSS 119
DB 61 NQFKSKATLVTKSTSTAVMELSLRSEPTAVYYCARQSD--YFPDYMGQGLTVTVSS 117
RESULT 5
AAV77596
ID AAV77596 standard; peptide; 136 AA.
XX AAV77596;
XX
XX 08-MAY-2000 (first entry)
XX Anti-human VEGF receptor Flt-1 antibody related peptide sequence #91.
XX Antibody; human; vascular endothelial growth factor; VEGF receptor;
XX Flt-1; neovascularisation; cell proliferation; metastasis; tumour;
XX rheumatoid arthritis; retinopathy; psoriasis.
XX Mus musculus.
XX OS
XX WO9600025-A1.
XX 25-NOV-1999.
XX 20-MAY-1999; 99WO-JP002661.
XX 20-MAY-1998; 98JP-00139000.
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX Shitara K, Ito M, Kawada Y, Nakamura K;
XX WPI; 2000-072431/06.
XX N-PSDB; AAZ8738.
XX Gene recombinant antibodies, useful for diagnosis and as remedies for PT diseases due to abnormal neovascularization e.g. proliferation or PT metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy and PT psoriasis.
XX Claim 28; Page 199-200; 210pp; Japanese.
XX

CC The invention relates to a gene recombinant antibody that has specific
 CC reaction with human vascular endothelial growth factor (VEGF) receptor
 CC Flt-1. The antibodies are useful for diagnosis and as remedies for
 CC diseases due to abnormal neovascularisation such as proliferation or
 CC metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic
 CC retinopathy, premature retinopathy and psoriasis
 CC
 SQ Sequence 136 AA;

Query Match 78.5%; Score 504; DB 3; Length 136;
 Best Local Similarity 80.7%; Pred. No. 1.7e-36;
 Matches 96; Conservative 9; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVQLVDSGAEVKKPKASVKISCKVGFATNYMHWVRQAPGKLEWIGYIDPYGDPGY 60
 DB 20 QVQLVDSGAEVKKPKASVAVSCASGYTIFINMHMVARQAPGQLEMMGALFPGNGFTSY 79
 QY 61 SQKFKGKATLTVDKSTSTAYMELSLRSEDYAVVYCARGNPFYFDYWGQGLTVTVSS 119
 DB 80 NQKFKGRVITVDKSTSTAYMELSLRSEDYAVVYCARGDG--YFPDYWGQGLTVTVSS 136

RESULT 6

AAB78865
 ID AAB78865 standard; protein; 136 AA.

XX AAB78865;

DT 20-APR-2001 (first entry)

DE Anti-human Flt-1 antibody VH CDR protein sequence SEQ ID 87.

KM Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;
 KM vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
 KM delayed hypersensitivity; malignant tumor; arteriosclerosis.

OS Synthetic.

XX WO200079275-A1.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-JP003957.

XX 17-JUN-1999; 99JP-00171709.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Shibuya M;

XX WPI; 2001-080847/09.

PT Substances binding to human vascular endothelial growth factor receptor
 PT Flt-1, used for diagnosis and treatment of inflammatory diseases,
 PT arteriosclerosis, cancer and delayed hypersensitivity.
 XX
 PS Example 3; Page 155; 164pp; Japanese.

CC This invention relates to a reagent for detecting differentiation of
 CC monocytes and macrophages from haematopoietic stem cells, containing a
 CC substance which binds to human vascular endothelial growth factor (VEGF)
 CC receptor Flt-1. The invention also includes a method for diagnosing a
 CC disease in which the differentiation of monocytes and macrophages is
 CC implicated, using the reagent, and an agent for the treatment of diseases
 CC diagnosed using the method, containing a substance which binds to Flt-1
 CC or a substance which inhibits the signal transduction of Flt-1. Diseases
 CC which may be diagnosed or treated include inflammation, delayed
 CC hypersensitivity, malignant tumours and arteriosclerosis. AAF70190 -
 CC AAF70244, AAF70251 and AAF70258 represent DNA sequences encoding anti-
 CC human Flt-1 monoclonal antibody fragments, and oligonucleotides used in
 CC the construction of the antibody. The monoclonal antibody is used in the
 CC reagent of the invention. PCR primers AAF70245 - AAF78870 (excluding
 CC AAF70251) are used in the isolation of the antibody DNA sequences.

CC Protein sequences AAB78848 - AAB78870 represent fragments of the anti-
 CC human Flt-1 antibody
 CC
 SQ Sequence 136 AA;

Query Match 78.5%; Score 504; DB 4; Length 136;
 Best Local Similarity 80.7%; Pred. No. 1.7e-36;
 Matches 96; Conservative 9; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVQLVDSGAEVKKPKASVKISCKVGFATNYMHWVRQAPGKLEWIGYIDPYGDPGY 60
 DB 20 QVQLVDSGAEVKKPKASVAVSCASGYTIFINMHMVARQAPGQLEMMGALFPGNGFTSY 79
 QY 61 SQKFKGKATLTVDKSTSTAYMELSLRSEDYAVVYCARGNPFYFDYWGQGLTVTVSS 119
 DB 80 NQKFKGRVITVDKSTSTAYMELSLRSEDYAVVYCARGDG--YFPDYWGQGLTVTVSS 136

RESULT 7

AAB84099
 ID AAB84099 standard; protein; 110 AA.

XX AAB84099;

DT 15-MAR-1999 (first entry)

DE Vitronectin alpha-v beta-3 MAb VH.

KM Humanised antibody; monoclonal antibody; MAb; antibody engineering;
 KM mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer;
 KM metastasis; rheumatoid arthritis; arteriosclerosis; angiogenesis;
 KM diabetic retinopathy; inflammation; macular degeneration; osteoporosis;
 KM Paget's disease; hyperparathyroidism; hypercalcaemia; therapy;
 KM immunotherapy.

XX Mus sp.

XX WO9840488-A1.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US004987.

XX 12-MAR-1997; 97US-0039609P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Jonak ZL, Johanson KO, Taylor AH;

XX WPI; 1999-034590/03.

PT New anti alpha v beta 3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory
 PT disorders, arteriosclerosis, restenosis, cancers or osteoporosis.
 XX
 PS Example 13; Page 63; 97pp; English.

CC This is the amino acid sequence of the region of the murine monoclonal
 CC antibody (MAb) D12 heavy chain variable region (VH) that is altered in
 CC humanised D12 VH (see also AAB84097). A synthetic gene (see AAB81901)
 CC encoding the protein was prepared from synthetic oligonucleotides and
 CC used to prepare an expression vector for humanised D12 VH. D12 is an anti
 CC -human alpha-v beta-3 vitronectin receptor MAb. Humanised D12 MAb can be
 CC used for passive immunotherapy of disorders mediated by the alpha-v beta-
 CC 3 vitronectin receptor, e.g. restenosis and angiogenic associated
 CC diseases

XX SQ Sequence 110 AA;

Query Match 78.3%; Score 503; DB 2; Length 110;
 Best Local Similarity 85.1%; Pred. No. 1.7e-36;
 Matches 97; Conservative 6; Mismatches 5; Indels 6; Gaps 2;

```

QY      3 QLVOSGAEVKKPGASVKISCKVSGYAFITNMVWVROAPGKLEWIGYIDPYGDPGY 62
DB      1 QLVOSGAEVKKPGASVKISCKVSGYAFITNMVWVROAPGKLEWIGYIDPYGDPGY 60
QY      63 KFKGKATLTVDKSTSTAYMELSLRSEDITAVYVCARR--GNFPYFPYWGQGT 114
DB      61 KFKGKATLTVDKSTSTAYMELSLRSEDITAVYVCARRGNYSFA----YWGQGT 110

RESULT 8
AAW29017 ID AAW29017 standard; protein; 135 AA.
XX      AAW29017;
AC      25-MAR-2003 (revised)
DT      30-MAR-1993 (first entry)
XX      pUC-RVh-1220d.
DE      Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KW      complementarity determining region; monoclonal; hybridoma; PCR; plasmid;
XX      polymerase chain reaction; amplify.
OS      Synthetic.
XX      Key
FH      Location/Qualifiers
FT      Peptide
FT      1..19
FT      /note="Leader peptide"
FT      Region
FT      20..49
FT      /label= FR1
FT      50..54
FT      /label= CDR1
FT      55..68
FT      /label= FR2
FT      69..85
FT      /label= CDR2
FT      Region
FT      86..117
FT      /label= FR3
FT      118..124
FT      /label= CDR3
FT      125..135
FT      Region
FT      /label= FR4

XX      WO9219759-A1.
XX      12-NOV-1992.
XX      24-APR-1992; 92WO-JP000544.
XX      25-APR-1991; 91JP-00095476.
XX      19-FEB-1992; 92JP-00032084.
XX      (CHUS ) CHUGAI SEIRYAKU KK.
XX      PA
XX      TSUCHIYA M, Sato K, Bendig MM, Jones ST, Saldanha JM;
XX      WPI; 1992-398882/48.
XX      DR N-PSDB; AAQ31391.
XX      PT Reconstituted human antibody to human interleukin-6 receptor - has low
XX      antigenicity and contains mouse V-region complementarity determining
XX      regions.
XX      PS Disclosure; Page 159-60; 207pp; Japanese.
XX      CC The sequences given in AAW29016-17 are portions of monoclonal antibodies
XX      which were encoded by plasmids contained within the mouse hybridoma,
XX      AOKI-20. The DNA encoding the complementarity determining regions
XX      (CDR's) was isolated by polymerase chain reaction. These antibodies
XX      recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were
XX      transformed with plasmids containing fragments of the antibody gene which

```

```

CC      caused the production of the antibody from the hybridoma cell line.
CC      (Updated on 25-MAR-2003 to correct PN field.)
XX      SQ Sequence 135 AA;
XX      Query Match          77.5%; Score 497.5; DB 2; Length 135;
XX      Best Local Similarity 79.0%; Pred. No. 6,2e-36;
XX      Matches 94; Conservative 11; Mismatches 11; Indels 3; Gaps 1;

QY      1 EVOLVOSGAEVKKPGASVKISCKVSGYAFITNMVWVROAPGKLEWIGYIDPYGDPGY 60
DB      20 QVQLVOSGAEVKKPGASVKISCKVSGYAFITNMVWVROAPGKLEWIGYIDPYGDPGY 79
QY      61 SOKFKGKATLTVDKSTSTAYMELSLRSEDITAVYVCARRGNFPYFPYWGQGT 119
DB      80 NQFKGKATLTVDKSTSTAYMELSLRSEDITAVYVCARRGN--RFAYWGQGT 135

RESULT 9
AAW22418 ID AAW22418 standard; protein; 116 AA.
XX      AAW22418;
AC      08-DEC-1997 (first entry)
DT      Reelaped human AUK12-20 VH.
XX      DE
XX      KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma;
XX      atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis;
XX      inflammatory bowel disease; rheumatoid arthritis; transplant rejection;
XX      graft versus host disease; nephritis; atopic dermatitis; psoriasis;
XX      myocardial ischaemia; acute leukocyte mediated lung injury; therapy;
XX      AUK12-20.
XX      KW
XX      OS Homo; sapiens.
XX      OS Synthetic.
XX      OS Chimeric.
XX      FH Key
XX      Location/Qualifiers
FT      Region
FT      1..30
FT      /label= FR1
FT      31..35
FT      Region
FT      36..49
FT      /label= CDR1
FT      50..66
FT      /label= FR2
FT      67..98
FT      /label= CDR2
FT      Region
FT      99..105
FT      /label= FR3
FT      106..116
FT      Region
FT      /label= FR4

XX      WO9718838-A1.
XX      29-MAY-1997.
XX      21-NOV-1996; 96WO-US018807.
XX      21-NOV-1995; 95US-00561521.
XX      (ATHB-) ATHENA NEUROSCIENCES INC.
XX      PA
XX      BENDIG MM, Leger OJ, Saldanha J, Jones ST, Yednock TA;
XX      WPI; 1997-297879/27.
XX      DR
XX      PT Uses of humanised alpha-4 integrin antibody - for treatment of asthma,
XX      atherosclerosis, AIDS, dementia, etc.
XX      PS Example 6; Page 44; 107pp; English.

```

XX This polypeptide comprises version 'b', of a reshaped human antibody
CC AUk2-20 VH region. A DNA fragment encoding the polypeptide was subcloned
CC into vector pUC19 for use as a template for PCR amplification and
CC production of version 'a' of a reshaped human 21.6 VH region (see
CC AAW22413) that can be used in the construction of novel humanised anti-
CC alpha-4 integrin antibodies. Claimed humanised antibodies are useful in
CC the treatment of asthma, atherosclerosis, AIDS, dementia, diabetes,
CC inflammatory bowel disease, rheumatoid arthritis, transplant rejection,
CC graft versus host disease, tumour metastasis, nephritis, atopic
CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated
CC lung injury
XX

SQ Sequence 116 AA;

Query Match 77.3%; Score 496.5; DB 2; Length 116;
Best Local Similarity 78.2%; Pred. No. 6.6e-36;

Matches 93; Conservative 12; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKISCKVSGVAFITNNMWWVQAQPGKLEWIGYIDPYGDPGY 60
DB 1 QVQLVQSGAEVKKPGASVKISCKVSGVAFITNNMWWVQAQPGKLEWIGYIDPYGDPGY 60
QY 61 SOKFKGKATLVVDKSTSTAYMELSLRSEDPAVYYCARGNFPYFDYWGQGLTVYSS 119
DB 61 NQKFKGKATLVVDKSTSTAYMELSLRSEDPAVYYCARGN---RFAYWGQGLTVYSS 116

RESULT 10

AAW29016
ID AAW29016 standard; protein; 135 AA.

AC AAW29016;

DT 25-MAR-2003 (revised)
DT 30-MAR-1993 (first entry)

DE pUC-RVh-1220b.

XX Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
KM complementarity determining region; monoclonal; hybridoma; PCR; plasmid;
KW polymerase chain reaction; amplify.

XX Synthetic.

FT Key Location/qualifiers
FT Peptide 1..19
FT /note= "Leader peptide"

FT Region 20..49
FT /label= FR1

FT Region 50..54
FT /label= CDR1

FT Region 55..68
FT /label= CDR2

FT Region 69..85
FT /label= FR2

FT Region 86..117
FT /label= CDR2

FT Region 118..124
FT /label= FR3

FT Region 125..135
FT /label= CDR3

FT Region 125..135
FT /label= FR4

XX WO9219759-A1.

XX 12-NOV-1992.

XX 24-APR-1992; 92WO-JP000544.

XX 25-APR-1991; 91JP-00095476.

XX 19-FEB-1992; 92JP-00032084.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JM;
PI WPI; 1992-398882/48.
DR N-PSDB; AAQ31391.

PT Reconstituted human antibody to human interleukin-6 receptor - has low
PT antigenicity and contains mouse V-region complementarily determining
PT regions.

XX Disclosure; Page 157-8; 207pp; Japanese.

XX The sequences given in AAW29016-17 are portions of monoclonal antibodies
CC which were encoded by plasmids contained within the mouse hybridoma,
CC AAK12-20. The DNA encoding the complementarity determining regions
CC (CDR's) was isolated by polymerase chain reaction. These antibodies
CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were
CC transformed with plasmids containing fragments of the antibody gene which
CC caused the production of the antibody from the hybridoma cell line.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 135 AA;

Query Match 77.3%; Score 496.5; DB 2; Length 135;
Best Local Similarity 78.2%; Pred. No. 7.6e-36;

Matches 93; Conservative 12; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVQLVQSGAEVKKPGASVKISCKVSGVAFITNNMWWVQAQPGKLEWIGYIDPYGDPGY 60
DB 20 QVQLVQSGAEVKKPGASVKISCKVSGVAFITNNMWWVQAQPGKLEWIGYIDPYGDPGY 79
QY 61 SOKFKGKATLVVDKSTSTAYMELSLRSEDPAVYYCARGNFPYFDYWGQGLTVYSS 119
DB 80 NQKFKGKATLVVDKSTSTAYMELSLRSEDPAVYYCARGN---RFAYWGQGLTVYSS 135

RESULT 11

AAW73187
ID AAW73187 standard; protein; 144 AA.

AC AAW73187;

DT 22-JAN-1999. (first entry)

DE Fragment of ganglioside GM2 targeting antibody.

XX Ganglioside GM2; antibody; complementarity determining region; cancer;
KM anti-tumour agent.

XX Homo sapiens.

OS JPL0257893-A.

PN 29-SEP-1998.

PD 19-MAR-1997; 97JP-00066981.

PR 19-MAR-1997; 97JP-00066981.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX WPI; 1998-575904/49.

XX N-PSDB; AAV08097.

XX A human type complementarity determining region transplanted antibody
PT against ganglioside GM2 - useful as an anti-tumour agent and as a
PT diagnostic for related cancers.

XX Example 4; Page 46-47; 66pp; Japanese.

XX This sequence is a fragment of an antibody of the invention. The antibody
CC of the invention is a human complementarity determining region
CC transplanted antibody that reacts specifically with ganglioside GM2. DNA

CC encoding the antibody, and vectors and transformants containing it, can
CC be used for the recombinant production of the antibody. The antibody
CC itself can be used as an anti-tumour agent or as a diagnostic tool for
CC related cancers. The antibody has antitumour activity against ganglioside
CC GM2 positive cells
XX
SQ Sequence 144 AA;

Query Match 76.7%; Score 492.5; DB 2; Length 144;
Best Local Similarity 80.0%; Pred. No. 1.8e-35;
Matches 96; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 EVQLVDSGAEVKKPKGASVKISCKVSGYAFITNYNMYWRQAPGKLEMTIGYIDPYGDPGY 60
DB 20 EVQLVDSGAEVKKPKGASVKISCKVSGYAFITNYNMYWRQAPGKLEMTIGYIDPYGDPGY 79
QY 61 SQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARNGN-FPYDPYWGQGLTVTVSS 119
DB 80 NQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCATYGHYGYMFAVWGQGLTVTVSS 139

RESULT 12

ADL1893
ID ADL1893 standard; peptide; 117 AA.

XX
AC ADL1893;

DT 06-MAY-2004 (first entry)

XX CDR transplant antibody heavy chain variable region #4.

KM cancer metastasis; human vascular endothelial growth factor; VEGF;
KW receptor Flt-1; Cytostatic; lung cancer; CDR.

XX Homo sapiens.

XX JP2003261460-A.

XX 16-SEP-2003.

XX 08-MAR-2002; 2002JP-00063835.

XX 08-MAR-2002; 2002JP-00063835.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX (SHIBU) SHIBUYA T.

XX WPI; 2004-056096/06.

PT Preventive or therapeutic agent of lung selective cancer metastasis
PT containing the substance which inhibits the information transmission
PT which intervenes human VEGF receptor Flt-1 as an active ingredient.

PS Claim 18; SEQ ID NO 20; 36pp; Japanese.

CC The present invention relates to a preventive or therapeutic agent of
CC lung selective cancer metastasis containing the substance which inhibits
CC the information transmission which intervenes human vascular endothelial
CC growth factor (VEGF) receptor Flt-1 as an active ingredient. The
CC invention is useful for inhibiting spread of lung cancer, and effectively
CC controls the spread of lung cancer. The present sequence represents a CDR
CC transplant antibody heavy chain variable region.

XX
SQ Sequence 117 AA;

Query Match 76.6%; Score 492; DB 8; Length 117;
Best Local Similarity 78.2%; Pred. No. 1.6e-35;
Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVQLVDSGAEVKKPKGASVKISCKVSGYAFITNYNMYWRQAPGKLEMTIGYIDPYGDPGY 60
DB 1 QVQLVDSGAEVKKPKGASVKISCKVSGYAFITNYNMYWRQAPGKLEMTIGYIDPYGDPGY 60

QY 61 SQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARNGNFPYDPYWGQGLTVTVSS 119
DB 61 NQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYFCARDG--YFPDYWGQGLTVTVSS 117

RESULT 13

AA77600
ID AA77600 standard; peptide; 136 AA.

XX
AC AA77600;

DT 08-MAY-2000 (first entry)

XX Anti-human VEGF receptor Flt-1 antibody related peptide sequence #95.

KM Antibody; human; vascular endothelial growth factor; VEGF receptor;
KW Flt-1; neovascularisation; cell proliferation; metastasis; tumour;
KW rheumatoid arthritis; retinopathy; psoriasis.

XX Mus musculus.

XX WO9960025-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99KO-JP002661.

XX 20-MAY-1998; 98JP-00139000.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Shitara K, Ito M, Kawada Y, Nakamura K;

XX WPI; 2000-072431/06.

XX N-PSDB; AAZ87778.

PT Gene recombinant antibodies, useful for diagnosis and as remedies for
PT diseases due to abnormal neovascularization e.g. proliferation or
PT metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy and
PT psoriasis.

PS Claim 28; Page 203; 210pp; Japanese.

CC The invention relates to a gene recombinant antibody that has specific
CC reaction with human vascular endothelial growth factor (VEGF) receptor
CC Flt-1. The antibodies are useful for diagnosis and as remedies for
CC diseases due to abnormal neovascularisation such as proliferation or
CC metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic
CC retinopathy, premature retinopathy and psoriasis

XX
SQ Sequence 136 AA;

Query Match 76.6%; Score 492; DB 3; Length 136;
Best Local Similarity 78.2%; Pred. No. 1.9e-35;
Matches 93; Conservative 11; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVQLVDSGAEVKKPKGASVKISCKVSGYAFITNYNMYWRQAPGKLEMTIGYIDPYGDPGY 60
DB 20 EVQLVDSGAEVKKPKGASVKISCKVSGYAFITNYNMYWRQAPGKLEMTIGYIDPYGDPGY 79
QY 61 SQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARNGNFPYDPYWGQGLTVTVSS 119
DB 80 NQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYFCARDG--YFPDYWGQGLTVTVSS 136

RESULT 14

AA78869
ID AA78869 standard; protein; 136 AA.

XX
AC AA78869;

DT 20-APR-2001 (first entry)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 18:05:34 ; Search time 68.8024 Seconds
(without alignments)
622.182 Million cell updates/sec

Title: US-10-774-076-12

Perfect score: 642
Sequence: 1 EVGLVSGAEVKKRPGASVKI.....GNFPYFDYWGQGLTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

.Published Applications AA:*

1: /cgn2_6/ptodaca/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodaca/2/pubpaa/PC7_NEW_PUB.pep:*

3: /cgn2_6/ptodaca/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodaca/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodaca/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodaca/2/pubpaa/PC7US_PUBCOMB.pep:*

7: /cgn2_6/ptodaca/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodaca/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodaca/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodaca/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodaca/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodaca/2/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodaca/2/pubpaa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodaca/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodaca/2/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodaca/2/pubpaa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodaca/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodaca/2/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodaca/2/pubpaa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodaca/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	642	100.0	119	17	US-10-774-076-12
2	642	100.0	138	17	US-10-774-076-17
3	564	87.9	119	17	US-10-774-076-2
4	564	87.9	138	17	US-10-774-076-9
5	530	82.6	117	14	US-10-223-880-5
6	504	78.5	136	14	US-10-160-232-91
7	503	78.3	110	14	US-10-223-880-12
8	492	76.6	136	14	US-10-160-232-95
9	490.5	76.4	135	9	US-09-249-011A-6
10	490.5	76.4	146	9	US-09-249-011A-24
11	488.5	76.1	116	14	US-10-389-155-16
12	488.5	76.1	116	15	US-10-389-417-16
13	488.5	76.1	116	15	US-10-452-357-57

14	486.5	75.8	118	14	US-10-148-844-43	Sequence 43, App1
15	483.5	75.3	116	14	US-10-127-890-169	Sequence 169, App
16	483.5	75.3	116	14	US-10-340-189-86	Sequence 86, App1
17	483.5	75.3	116	14	US-10-389-155-25	Sequence 25, App1
18	483.5	75.3	116	15	US-10-325-696-55	Sequence 55, App1
19	483.5	75.3	116	15	US-10-389-417-25	Sequence 25, App1
20	483.5	75.3	135	14	US-10-389-155-32	Sequence 32, App1
21	483.5	75.3	135	15	US-10-389-417-32	Sequence 32, App1
22	483.5	75.3	135	15	US-10-452-357-19	Sequence 19, App1
23	483.5	75.3	139	9	US-09-760-723-7	Sequence 7, App1
24	483.5	75.3	139	9	US-09-760-723-8	Sequence 8, App1
25	483.5	75.3	139	9	US-09-355-925-7	Sequence 7, App1
26	483.5	75.3	139	9	US-09-355-925-8	Sequence 8, App1
27	483.5	75.3	139	10	US-09-269-921-125	Sequence 125, App
28	483.5	75.3	139	10	US-09-269-921-128	Sequence 128, App
29	483.5	75.3	139	10	US-09-509-098-50	Sequence 50, App1
30	483.5	75.3	139	10	US-09-509-098-127	Sequence 127, App
31	483.5	75.3	139	14	US-10-315-125-7	Sequence 7, App1
32	483.5	75.3	139	14	US-10-315-125-8	Sequence 8, App1
33	483.5	75.3	139	14	US-10-218-253-125	Sequence 125, App
34	483.5	75.3	139	14	US-10-218-253-128	Sequence 128, App
35	483.5	75.3	139	14	US-10-428-085-7	Sequence 7, App1
36	483.5	75.3	139	14	US-10-428-085-8	Sequence 8, App1
37	483.5	75.3	139	16	US-10-474-714-6	Sequence 6, App1
38	483	75.2	117	9	US-09-956-206A-78	Sequence 78, App1
39	483	75.2	136	9	US-09-956-206A-63	Sequence 63, App1
40	483	75.2	448	9	US-09-917-410-6	Sequence 6, App1
41	482.5	75.2	139	10	US-09-269-921-111	Sequence 111, App
42	482.5	75.2	139	10	US-09-269-921-117	Sequence 117, App
43	482.5	75.2	139	10	US-09-509-098-22	Sequence 22, App1
44	482.5	75.2	139	10	US-09-509-098-34	Sequence 34, App1
45	482.5	75.2	139	14	US-10-218-253-111	Sequence 111, App

ALIGNMENTS

RESULT 1

US-10-774-076-12

; Sequence 12, Application US/10774076

; Publication No. US20040210040A1

; GENERAL INFORMATION:

; APPLICANT: Protein Design Labs, Inc.

; TITLE OF INVENTION: Antiherpetic Antibodies and Their Use to Treat Cancer and

; TITLE OF INVENTION: Proteinase

; FILE REFERENCE: 05882.0064.NPUS01

; CURRENT APPLICATION NUMBER: US/10/774,076

; CURRENT FILING DATE: 2004-02-06

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 12

; LENGTH: 119

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Humanized antibody

US-10-774-076-12

Query Match 100.0%; Score 642; DB 17; Length 119;

Best Local Similarity 100.0%; Pred. No. 8.6e-52;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVGLVSGAEVKKRPGASVKISCRVSGYAFNTNMVWYRQAPGKLEWIGIDYDGPY 60

1 EVGLVSGAEVKKRPGASVKISCRVSGYAFNTNMVWYRQAPGKLEWIGIDYDGPY 60

DB 61 SORFKKATITVTKSSTAYMELSSLRSEPTATYYCARRNPFYFDYWGQGLTVSS 119

QY 61 SORFKKATITVTKSSTAYMELSSLRSEPTATYYCARRNPFYFDYWGQGLTVSS 119

DB 61 SORFKKATITVTKSSTAYMELSSLRSEPTATYYCARRNPFYFDYWGQGLTVSS 119

RESULT 2

US-10-774-076-17
; Sequence 17, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-10-774-076-17

Query Match 100.0%; Score 642; DB 17; Length 138;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPKGASVKISCKVSGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 60
DB 20 EVQLVQSGAEVKKPKGASVKISCKVSGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 79
QY 61 SQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARRGNPFYFDYWGQGLTVTVSS 119
DB 80 SQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARRGNPFYFDYWGQGLTVTVSS 138

RESULT 3
US-10-774-076-2
; Sequence 2, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-2

Query Match 87.9%; Score 564; DB 17; Length 119;
Best Local Similarity 84.9%; Pred. No. 1.4e-44;
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPKGASVKISCKVSGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 60
DB 1 EIQLQSGPELVKPGASVKVSCASGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 60
QY 61 SQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARRGNPFYFDYWGQGLTVTVSS 119
DB 61 SQKFKGKATLTVDKSSSTAYMELSLRSEDAVYYCARRGNPFYFDYWGQGLTVTVSS 119

RESULT 4
US-10-774-076-9
; Sequence 9, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.

; APPLICANT: Landolfi, et al.
; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Psoriasis
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 138
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-9

Query Match 87.9%; Score 564; DB 17; Length 138;
Best Local Similarity 84.9%; Pred. No. 1.7e-44;
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVQLVQSGAEVKKPKGASVKISCKVSGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 60
DB 20 EIQLQSGPELVKPGASVKVSCASGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 79
QY 61 SQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARRGNPFYFDYWGQGLTVTVSS 119
DB 80 SQKFKGKATLTVDKSSSTAYMELSLRSEDAVYYCARRGNPFYFDYWGQGLTVTVSS 138

RESULT 5
US-10-223-880-5
; Sequence 5, Application US/10223880
; Publication No. US20030152571A1
; GENERAL INFORMATION:
; APPLICANT: JONAK, ZDENKA
; APPLICANT: JOHANSON, KYUNG O.
; APPLICANT: TAYLOR, ALEXANDER
; TITLE OF INVENTION: ANIT-ALPHAETA3 HUMANIZED MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: P50629C1
; CURRENT APPLICATION NUMBER: US/10/223,880
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 09/380,910
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/04987
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/039,609
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-880-5

Query Match 82.6%; Score 530; DB 14; Length 117;
Best Local Similarity 85.1%; Pred. No. 1.9e-41;
Matches 103; Conservative 7; Mismatches 5; Indels 6; Gaps 2;

QY 1 EVQLVQSGAEVKKPKGASVKISCKVSGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 60
DB 1 QVQLVQSGAEVKKPKGASVKVSCASGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 60
QY 61 SQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCAR--GNFPYFDYWGQGLTVTVSS 118
DB 61 NQKFKGKATLTVDKSTSTAYMELSLRSEDTAVYYCARQNYGSAFA---YWGQGLTVTVSS 116

RESULT 6
US-10-160-232-91

```

: Sequence 91 Application US/10160232
: Publication No. US20030088075A1
: GENERAL INFORMATION:
: APPLICANT: SHITARA, KENYA
: APPLICANT: ITO, MIKITO
: APPLICANT: HANAI, NOBUO
: APPLICANT: KAWADA, YOKO
: APPLICANT: MAKAMURA, KAZUYASU
: APPLICANT: SHIBUYA, MASAHUMI
: TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
: FILE REFERENCE: 249-107
: CURRENT APPLICATION NUMBER: US/10/160,232
: PRIOR FILING DATE: 2002-06-04
: PRIOR APPLICATION NUMBER: US/09/453,718
: PRIOR FILING DATE: 1999-12-03
: PRIOR APPLICATION NUMBER: 09/315,051
: PRIOR FILING DATE: 1999-05-20
: PRIOR APPLICATION NUMBER: 09/119,014
: PRIOR FILING DATE: 1998-07-20
: PRIOR APPLICATION NUMBER: PCT/JP97/04259
: PRIOR FILING DATE: 1997-11-21
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 91
: LENGTH: 136
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
: US-10-160-232-91

```

Query Match	78.5%;	Score 504;	DB 14;	Length 136;
Best Local Similarity	80.7%;	Pred. No. 5.8e-39;		
Matches 96;	Conservative 9;	Mismatches 12;	Indels 2;	Gaps 1;

[illegible]

RESULT 7
US-10-223-880-12
; Sequence 12, Application US/10223880
; Publication No. US20030152571A1

```

1  APPLICANT: JONAK, ZDENKA
2  APPLICANT: JOHANSON, KYUNG O.
3  APPLICANT: TAYLOR, ALEXANDER
4  TITLE OF INVENTION: ANTI-ALPHAETA3 HUMANIZED MONOCLONAL
5  TITLE OF INVENTION: ANTIBODIES
6  FILE REFERENCE: P50629C1
7  CURRENT APPLICATION NUMBER: US/10/223,880
8  CURRENT FILING DATE: 2002-08-20
9  PRIOR APPLICATION NUMBER: 09/380,910
10 PRIOR FILING DATE: 1999-09-10
11 PRIOR APPLICATION NUMBER: PCT/US98/04987
12 PRIOR FILING DATE: 1998-03-12
13 PRIOR APPLICATION NUMBER: 60/039,609
14 PRIOR FILING DATE: 1997-03-12
15 NUMBER OF SEQ ID NOS: 45
16 SOFTWARE: FASTSEQ for Windows Version 4.0
17 SEQ ID NO 12
18 LENGTH: 110
19 TYPE: PRT
20 ORGANISM: Mus musculus
21 US-10-223-880-12

```

Query Match	78.3%;	Score 503;	DB 14;	Length 110;
Best Local Similarity	85.1%;	Pred. No. 5.8e-39;		

Matches 97; Conservative 6; Mismatches 5; Indels 6; Gaps 2;

Qy 3 QLVOSGLEVKKPKGASVYISCKVSGVAFPTNNMTWVAQAQKGLGEMVGYIDPPYSGPGVYSQ 62
Db 1 QLVOSGLEVKKPKGASVYVSCSKASGAFPTSNMTWVAQAQGLGEMVGYIDPPNGDPTFNQ 60
Qy 63 KFKGKATLTVDKSTSTANMELSLRSEDPAVYTCARR--GNPYYTYDNGQGTLL 114
Db 61 KFKGKATLTVDKSTSTANMELSLRSEDPAVYTCARQNGSFA----YNGQGTLL 110

RESULT 8
US-10-160-232-95

```

? Sequence 95, Application US/10160232
? Publication No. US20030088075A1
?
? GENERAL INFORMATION:
? APPLICANT: SHITARA, KENYA
? APPLICANT: ITO, MIKITO
? APPLICANT: HANAI, NOBUO
? APPLICANT: KAWADA, YOKO
? APPLICANT: NAKAMURA, KATUYASU
? APPLICANT: SHIBUYA, MASABUMI
? TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
? FILE REFERENCE: 249-107
? CURRENT APPLICATION NUMBER: US/10/160,232
? CURRENT FILING DATE: 2002-06-04
? PRIOR APPLICATION NUMBER: US/09/453,718
? PRIOR FILING DATE: 1999-12-03
? PRIOR APPLICATION NUMBER: 09/315,051
? PRIOR FILING DATE: 1999-05-20
? PRIOR APPLICATION NUMBER: 09/119,014
? PRIOR FILING DATE: 1998-07-20
? PRIOR APPLICATION NUMBER: PCT/JP97/04259
? PRIOR FILING DATE: 1997-11-21
? NUMBER OF SEQ ID NOS: 96
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 95
?
? LENGTH: 136
? TYPE: PR1
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
? US-10-160-232-95

```

Query Match	76.6%;	Score 492;	DB 14;	Length 136;
Best Local Similarity	-78.2%;	Pred. No. 7.5e-38;		
Matches	93;	Conservative	11;	Mismatches 13;
				Indels 2;
				Gaps 1;

[illegible]

RESULT 9
US-09-249-011A-6
; Sequence 6, Application US/09249011A

1 VASQUEZ, MAXIMILIANO
2
3 APPLICANT: CARRERO, BEATRIZ
4 APPLICANT: CENATIER, ABBIE CHERYLYN
5 APPLICANT: COLLINS, MARY
6 APPLICANT: GOLDMAN, SAUEL
7 GRAY, GARY S.
8 APPLICANT: KNIGHT, ANDEKA
9 APPLICANT: O'HARA, DENISE
10 APPLICANT:
11 APPLICANT:
12 APPLICANT: RUP, BONITA
13 VELDAM, GEERTUUDA M.

;; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
;; TITLE OF INVENTION: OF TREATMENT THEREWITH
;; FILE REFERENCE: 08702.0081-00000
;; CURRENT APPLICATION NUMBER: US/09/249,011A
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 6
;; LENGTH: 135
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Humanized
;; OTHER INFORMATION: murine anti-human B7-2 heavy chain
US-09-249-011A-6

Query Match 76.4%; Score 490.5; DB 9; Length 135;
Best Local Similarity 78.2%; Pred. No. 1e-37;
Matches 93; Conservative 11; Mismatches 12; Indels 3; Gaps 1;

QY 1 EVQLVDSGAEVKKPKASVKISCKVGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 60
DB 20 QVQLVDSGAEVKKPKGSSVKVSKASGTFITDYAIQWRQAPGQGLEWIGVINYIDNTNY 79
QY 61 SQRKRGATLTVDKSTSTAYMELSLRSEDTAVYTCARRGNFPYFDYWGQGLTVTVSS 119
DB 80 NQKFKGKATMTVDKSTSTAYMELSLRSEDTAVYTCARRA---WYMDYWGQGLTVTVSS 135

RESULT 10

US-09-249-011A-24
;; Sequence 24, Application US/09249011A
;; Patent No. US20020176855A1
;; GENERAL INFORMATION:
;; APPLICANT: CO, MAN SUNG
;; APPLICANT: VASQUEZ, MAXIMILIANO
;; APPLICANT: CARRENO, BEATRIZ
;; APPLICANT: CELINIKER, ABBIE CHERYL
;; APPLICANT: COLLINS, MARY
;; APPLICANT: GOLDMAN, SAMUEL
;; APPLICANT: GRAY, GARY S.
;; APPLICANT: KNIGHT, ANDREA
;; APPLICANT: O'HARA, DENISE
;; APPLICANT: RUP, BONITA
;; APPLICANT: VELDMAN, GEERTRUIDA M.
;; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
;; TITLE OF INVENTION: OF TREATMENT THEREWITH
;; FILE REFERENCE: 08702.0081-00000
;; CURRENT APPLICATION NUMBER: US/09/249,011A
;; CURRENT FILING DATE: 1999-02-12
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 24
;; LENGTH: 461
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-09-249-011A-24

Query Match 76.4%; Score 490.5; DB 9; Length 461;
Best Local Similarity 78.2%; Pred. No. 3.7e-37;
Matches 93; Conservative 11; Mismatches 12; Indels 3; Gaps 1;
QY 1 EVQLVDSGAEVKKPKASVKISCKVGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 60
DB 20 QVQLVDSGAEVKKPKGSSVKVSKASGTFITDYAIQWRQAPGQGLEWIGVINYIDNTNY 79
QY 61 SQRKRGATLTVDKSTSTAYMELSLRSEDTAVYTCARRGNFPYFDYWGQGLTVTVSS 119
DB 80 NQKFKGKATMTVDKSTSTAYMELSLRSEDTAVYTCARRA---WYMDYWGQGLTVTVSS 135

RESULT 11

US-10-389-155-16

;; Sequence 16, Application US/10389155
;; Publication No. US20030229208A1
;; GENERAL INFORMATION:
;; APPLICANT: Queen, Cary L.
;; Co, Man Sung
;; Schneider, William P.
;; Landolfi, Nicholas F.
;; Coeligh, Kathleen L.
;; Selick, Harold E.
;; TITLE OF INVENTION: Improved Humanized Immunoglobulins
;; NUMBER OF SEQUENCES: 100
;; CORRESPONDENCE ADDRESS:
;; ADDRESSER: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/389,155
;; FILING DATE: 13-Mar-2003
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/325,000
;; FILING DATE: 01-JUN-1999
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; APPLICATION NUMBER: US 07/310,252
;; FILING DATE: 13-FEB-1989
;; APPLICATION NUMBER: US 07/590,274
;; FILING DATE: 28-SEP-1990
;; APPLICATION NUMBER: US 07/634,278
;; FILING DATE: 19-DEC-1990
;; APPLICATION NUMBER: US 08/484,537
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 011823-002650US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 116 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: 1linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-389-155-16

Query Match 76.1%; Score 488.5; DB 14; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-37;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVQLVDSGAEVKKPKASVKISCKVGYAFITNNMWRQAPGKGLIEWIGYIDPYGDPGY 60
DB 1 QVQLVDSGAEVKKPKGSSVKVSKASGTFITDYNHWWRQAPGQGLEWIGYIIPYNGGTGY 60
QY 61 SQRKRGATLTVDKSTSTAYMELSLRSEDTAVYTCARRGNFPYFDYWGQGLTVTVSS 119
DB 61 NQKFKGKATITADSTSTAYMELSLRSEDTAVYTCARR--GRP--AMDYWGQGLTVTVSS 116

RESULT 12

US-10-389-417-16
;; Sequence 16, Application US/10389417
;; Publication No. US20040049014A1


```

; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; Co, Man Sung
; Schneider, William P.
; Landolfi, Nicholas P.
; Coelingh, Kathleen L.
; Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/389,417
; FILING DATE: 13-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,000
; FILING DATE: 01-JUN-1999
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; APPLICATION NUMBER: US 07/534,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 08/484,537
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-002650US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-389-417-16

Query Match          76.1%; Score 488.5; DB 15; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-37;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLVSGAEVKKPGASVKISCKVSGYAFITNNMYWROAPGKLEWIGYIDPYGPGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGAEVKKPGSSVKISCKASGTTFTDYNMHWRQAPGQGLEWIGITIPYNGSTGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 SQRKSKATLTVDKSTSTAYMELSLRSEDTAVYYCARNGNPFYFDYWGQGLTVTVSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQFKSKATTTADSTMTAYMELSLRSEDTAVYYCAR--GRP-ANDYWGQGLTVTVSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
US-10-452-357-57
; Sequence 57, Application US/10452357
; Publication No. US20040058414A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Queen, Cary
; APPLICANT: Co, Man Sung
; APPLICANT: Schneider, William
; APPLICANT: Landolfi, Nicholas
; APPLICANT: Coelingh, Kathleen
; APPLICANT: Selick, Harold
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; FILE REFERENCE: 05882.0078, CNUS01
; CURRENT APPLICATION NUMBER: US/10/452,357
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/718,993
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 09/487,200
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/634,278
; PRIOR FILING DATE: 1990-12-19
; PRIOR APPLICATION NUMBER: 07/590,275
; PRIOR FILING DATE: 1990-09-28
; PRIOR APPLICATION NUMBER: 07/310,252
; PRIOR FILING DATE: 1989-02-13
; PRIOR APPLICATION NUMBER: 07/290,975
; PRIOR FILING DATE: 1988-12-28
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patent version 3.2
; SEQ ID NO 57
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: humanized M195 heavy chain antibody
US-10-452-357-57
```

```

Query Match          76.1%; Score 488.5; DB 15; Length 116;
Best Local Similarity 79.0%; Pred. No. 1.3e-37;
Matches 94; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 1 EVOLVSGAEVKKPGASVKISCKVSGYAFITNNMYWROAPGKLEWIGYIDPYGPGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVSGAEVKKPGSSVKISCKASGTTFTDYNMHWRQAPGQGLEWIGITIPYNGSTGY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 SQRKSKATLTVDKSTSTAYMELSLRSEDTAVYYCARNGNPFYFDYWGQGLTVTVSS 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQFKSKATTTADSTMTAYMELSLRSEDTAVYYCAR--GRP-ANDYWGQGLTVTVSS 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
US-10-148-844-43
; Sequence 43, Application US/10148844
; Publication No. US20030096403A1
; GENERAL INFORMATION:
; APPLICANT: Hye-Jeong Hong
; APPLICANT: Keun-Soo Kim
; TITLE OF INVENTION: A HUMANIZED ANTIBODY TO SURFACE ANTIGEN S OF HEPATITIS B
; FILE REFERENCE: 118.15-US-WO
; CURRENT APPLICATION NUMBER: US/10/148,844
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: KR 2000-57891
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: KR 2001-60966
; PRIOR FILING DATE: 2001-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens Hzs-III-VH
US-10-148-844-43

Query Match          75.8%; Score 486.5; DB 14; Length 118;
Best Local Similarity 77.9%; Pred. No. 2.1e-37;
Matches 95; Conservative 7; Mismatches 13; Indels 7; Gaps 2;
```

Qy 1 EVOLVQSGAEVKKPGASVKISCKVSGYAFNTNMTWROAPGKLEWIGYIDPYGDPgy 60
Db 1 EVQLVQSGAEVKKPGASVKISCKVSGYFTFDYNNQWRAQAPGKLEWIGYIPYSGGTgy 60
Qy 61 SQKFGKATITVDKSTSTAYMELSLRSEDPAVYVCARGNPPYFPD---YWGQGLTVTV 117
Db 61 SQKFGKATITVDKSTSTAYMELSLRSEDPAVYVCARGNPPYFPD---YWGQGLTVTV 116
Qy 118 SS 119
Db 117 SS 118

RESULT 15

US-10-127-890-169
; Sequence 169, Application US/10127890
; Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-10-127-890-169

Query Match 75.3%; Score 483.5; DB 14; Length 116;
Best Local Similarity 77.3%; Pred. No. 3,9e-37;
Matches 92; Conservative 11; Mismatches 13; Indels 3; Gaps 1;

Qy 1 EVOLVQSGAEVKKPGASVKISCKVSGYAFNTNMTWROAPGKLEWIGYIDPYGDPgy 60
Db 1 EVQLVQSGAEVKKPGASVKISCKVSGYFTFDYNNQWRAQAPGKLEWIGYIPYSGGTgy 60
Qy 61 SQKFGKATITVDKSTSTAYMELSLRSEDPAVYVCARGNPPYFPDYGQGLTVTVSS 119
Db 61 NQKFKDKATITADESTNTAYMELSLRSEDPAVYVCARGG---VFDYWGQGLTVTVSS 116

Search completed: December 29, 2004, 18:42:00
Job time : 68.8024 secs

PI Epenetos AA, Spooner RA, Deonaraian M;
XX WPI; 1994-248907/30.
DR N-PSDB; AAQ070660.
XX
PT New cpds. comprising a targeting portion and a cytotoxic portion - used
PT esp. for treating mammals for destroying target cells, partic. tumour
PT cells.
XX
PS Disclosure; Fig 10; 114pp; English.
XX
CC The sequence is that of the SCFV pRAS109 and pRAS113 between HindIII and
CC EcoRI site obtd. by PCR. See also AAR56482-5. (Updated on 25-MAR-2003 to
CC correct FN field.)
XX
SQ Sequence 415 AA;
Query Match 97.0%; Score 559; DB 2; Length 415;
Best Local Similarity 97.3%; Pred. No. 5e-39;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QAVTQESALTTSPGEITVTLTGRSGAVTTSSNANVQEKPDHLPGLIGGTINRPGV 60
DB 158 QAVTQESALTTSPGEITVTLTGRSGAVTTSSNANVQEKPDHLPGLIGGTINRABGV 217
QY 61 PARFSGSLIGDKALTTTGAQTEDEAIYFCALMTSNHVPFGGTRKLTVLG 110
DB 218 PARFSGSLIGDKALTTTGAQTEDEAIYFCALMTSNHVPFGGTRKLTVLG 267
RESULT 4
AAR56482
ID AAR56482 standard; protein; 269 AA.
XX
AC AAR56482;
XX
DT 25-MAR-2003 (revised)
DT 26-MAR-1995 (first entry)
XX
DE SCFV pRAS107 and pRAS111.
XX
KW Amplification; single chain variable region fusion protein; PCR.
XX
OS Synthetic.
XX
FN WO9415644-A1.
XX
PD 21-JUL-1994.
XX
PF 17-JAN-1994; 94WO-GB000087.
XX
PR 15-JAN-1993; 93GB-00000686.
XX
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI Epenetos AA, Spooner RA, Deonaraian M;
XX
DR WPI; 1994-248907/30.
DR N-PSDB; AAQ056482.
XX
PT New cpds. comprising a targeting portion and a cytotoxic portion - used
PT esp. for treating mammals for destroying target cells, partic. tumour
PT cells.
XX
PS Disclosure; Fig 4; 114pp; English.
XX
CC The sequence is that of the SCFV pRAS107 and pRAS111 between HindIII and
CC EcoRI site obtd. by PCR. See also AAR56482-5. (Updated on 25-MAR-2003 to
CC correct FN field.)
XX
SQ Sequence 269 AA;
Query Match 96.5%; Score 556; DB 2; Length 269;

Best Local Similarity 96.4%; Pred. No. 5.7e-39;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 QAVTQESALTTSPGEITVTLTGRSGAVTTSSNANVQEKPDHLPGLIGGTINRPGV 60
DB 158 QAVTQESALTTSPGEITVTLTGRSGAVTTSSNANVQEKPDHLPGLIGGTINRABGV 217
QY 61 PARFSGSLIGDKALTTTGAQTEDEAIYFCALMTSNHVPFGGTRKLTVLG 110
DB 218 PARFSGSLIGDKALTTTGAQTEDEAIYFCALMTSNHVPFGGTRKLTVLG 267
RESULT 5
AAR09422
ID AAR09422 standard; protein; 131 AA.
XX
AC AAR09422;
XX
DT 25-MAR-2003 (revised)
DT 04-MAR-1993 (first entry)
XX
DE Br-3 Light Chain V Region (mouse).
XX
KW Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
KW antigen; diagnosis; cancer; tumour.
XX
OS Mus musculus.
XX
FN WO9002569-A.
XX
PD 22-MAR-1990.
XX
PF 08-SEP-1988; 88US-00241744.
XX
PR 08-SEP-1988; 88US-00241744.
PR 13-SEP-1988; 88US-00243739.
PR 04-OCT-1988; 88US-00253002.
PR 19-JUN-1989; 89US-00367641.
PR 21-JUL-1989; 89US-00382768.
XX
PA (ITGE-) INT GENETIC ENG INC.
PA (INGE-) INGENE INT GENETIC.
XX
PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX
DR WPI; 1990-115825/15.
DR N-PSDB; AAQ08604.
XX
PT Chimeric mouse-human antibodies - prepd. using genes coding for constant
PT human region murine variable region, esp. to 3 tumour antigen.
XX
PS Claim 13; Page 123 + Fig 14; 173pp; English.
XX
CC The sequence is used in the prodn. of a chimeric antibody mol. comprising
CC two light chains and two heavy chains, each having a constant region
CC (human) and a variable region (murine) having specificity to an antigen
CC bound by murine monoclonal antibody (Mab) Br-3. The chimeric antibodies
CC can be used for any purpose for which the original murine Mabs can be
CC used, with the advantage that they are more compatible with the human
CC body. They are esp. used for the diagnosis and treatment of cancer.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 131 AA;
Query Match 96.4%; Score 555; DB 2; Length 131;
Best Local Similarity 96.4%; Pred. No. 3.2e-39;
Matches 106; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 QAVTQESALTTSPGEITVTLTGRSGAVTTSSNANVQEKPDHLPGLIGGTINRPGV 60
DB 20 QAVTQESALTTSPGEITVTLTGRSGAVTTSSNANVQEKPDHLPGLIGGTINRABGV 79
QY 61 PARFSGSLIGDKALTTTGAQTEDEAIYFCALMTSNHVPFGGTRKLTVLG 110

Db 80 PARFSSGLIDKXALITITGTQTEDEALIFCALWYSNHWVGSGTKLTVLG 129

RESULT 6

ID AAW06211 standard; protein; 131 AA.

XX AAW06211;

DT 25-MAR-2003 (revised)

DT 12-FEB-1997 (first entry)

DE MAb Br-3 light chain variable region.

KM Chimeric antibody; monoclonal antibody; Br-3; antibody engineering;
KM tumour; antigen; breast carcinoma; lung carcinoma; colon carcinoma;
KM ovary carcinoma; cancer; diagnosis; therapy; light chain.

OS Mus sp.

PN US5576184-A.

PD 19-NOV-1996.

PF 27-DEC-1994; 94US-00364001.

PR 06-SEP-1988; 88US-00240624.

PR 08-SEP-1988; 88US-00241744.

PR 13-SEP-1988; 88US-00243739.

PR 04-OCT-1988; 88US-00253002.

PR 19-JUN-1989; 89US-00367641.

PR 21-JUL-1989; 89US-00382768.

PR 06-MAY-1991; 91US-00659401.

XX (XOMA) XOMA CORP.

PI Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;

XX WPI; 1997-011249/01.

DR N-PSDB; AAT43436.

XX Chimeric mouse-human antibodies - recognise a human tumour antigen, used

PT for the treatment and diagnosis of human cancers.

XX Example 3; Fig 14; 102pp; English.

PS The light chain variable region (AAW06211) of mouse monoclonal antibody

CC Br-3 is the product of a cDNA clone (AAT43436) isolated from a Br-3

CC hybridoma cDNA library. MAb Br-3 (IgG1) binds to an antigen that is

CC expressed on the surface of human lung, breast, colon and ovary

CC carcinomas, but not on most normal adult tissues. The light chain and

CC heavy chain variable regions (see also AAW06212) of B38-1 can be linked

CC to human constant regions and expressed in transformed host cells. Novel

CC mouse-human chimeric antibodies (see also AAW06209-10 and AAW06213-18)

CC can be produced that have specificity to human tumour antigens and can be

CC used for the treatment and diagnosis of human cancer. (Updated on 25-MAR-

CC 2003 to correct PF field.)

SQ Sequence 131 AA;

Query Match 96.4%; Score 555; DB 2; Length 131;

Best Local Similarity 96.4%; Pred. No. 3.2e-39;

Matches 106; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QAVVTGSSALTTSGETVTLTCRSSGAVTTSNANWVQEKDPDLFTGLIGTINRPGV 60

DB 20 QAVVTGSSALTTSGETVTLTCRSSGAVTTSNANWVQEKDPDLFTGLIGTINRPGV 79

QY 61 PARFSSGLIDKXALITITGTQTEDEALIFCALWYSNHWVGSGTKLTVLG 110

DB 80 PARFSSGLIDKXALITITGTQTEDEALIFCALWYSNHWVGSGTKLTVLG 129

RESULT 7

ID AAW85058 standard; protein; 131 AA.

XX AAW85058;

DT 20-MAR-2003 (revised)

DT 16-APR-1999 (first entry)

DE Mouse Br-3 heavy chain variable region.

KM Heavy chain variable region; murine antibody Br-3; antibody ING-1;
KM chimeric immunoglobulin; human tumour antigen; chimeric antibody;
KM treatment; human cancer.

OS Mus sp.

PN US5843685-A.

PD 01-DEC-1998.

PF 06-JUN-1995; 95US-00466034.

PR 06-SEP-1988; 88US-00240624.

PR 08-SEP-1988; 88US-00241744.

PR 13-SEP-1988; 88US-00243739.

PR 04-OCT-1988; 88US-00253002.

PR 19-JUN-1989; 89US-00367641.

PR 21-JUL-1989; 89US-00382768.

PR 06-SEP-1989; 89US-00382768.

PR 06-MAY-1991; 91US-00659401.

PR 27-DEC-1994; 94US-00364001.

XX (XOMA) XOMA CORP.

PI Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;

XX WPI; 1999-044574/04.

DR N-PSDB; AAV71154.

XX Chimeric antibody specific for human tumour antigen - useful as

PT immunosassay, imaging or antitumour agent.

XX Example 3; Fig 14; 92pp; English.

PS The present sequence represents the heavy chain variable region of murine

CC antibody Br-3. The sequence was used to create chimeric mouse-human

CC immunoglobulins which recognise the human tumour antigen bound by

CC antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The

CC chimeric antibodies also have an antigen-binding site that competitively

CC inhibits the binding of antibody ING-1, and mediate complement-dependent

CC cytotoxicity of target cells or antibody-dependent cellular cytotoxicity to

CC target cells. The chimeric antibodies can be used for therapeutic

CC purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to

CC correct PR field.)

SQ Sequence 131 AA;

Query Match 96.4%; Score 555; DB 2; Length 131;

Best Local Similarity 96.4%; Pred. No. 3.2e-39;

Matches 106; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QAVVTGSSALTTSGETVTLTCRSSGAVTTSNANWVQEKDPDLFTGLIGTINRPGV 60

DB 20 QAVVTGSSALTTSGETVTLTCRSSGAVTTSNANWVQEKDPDLFTGLIGTINRPGV 79

QY 61 PARFSSGLIDKXALITITGTQTEDEALIFCALWYSNHWVGSGTKLTVLG 110

DB 80 PARFSSGLIDKXALITITGTQTEDEALIFCALWYSNHWVGSGTKLTVLG 129

RESULT 8

ABUS8892
ID ABUS8892 standard; protein; 131 AA.
XX
AC ABUS8892;
XX
DT 16-APR-2003 (first entry)
XX
DE Mouse antibody light chain variable region #2.
XX
KM Mouse; human tumour antigen; anti-human tumour antigen-antibody;
KM ING-1 antibody; cell line HB912; immunoassay; imaging; tumour diagnosis;
KM tumour therapy; cytostatic; light chain variable region.
XX
OS Mus sp.
XX
PN US6461824-B1.
XX
PD 08-OCT-2002.
XX
PE 06-JUN-1995; 95US-00467142.
XX
PF 06-SEP-1988; 88US-00240624.
PR 08-SEP-1988; 88US-00241744.
PR 13-SEP-1988; 88US-00243739.
PR 04-OCT-1988; 88US-00253002.
PR 19-JUN-1989; 89US-00367641.
PR 21-JUL-1989; 89US-00382768.
PR 06-SEP-1989; 89MO-US003852.
PR 06-MAY-1991; 91US-00659401.
PR 27-DEC-1994; 94US-00364001.
XX
PA (XOMA) XOMA TECHNOLOGY LTD.
XX
PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP,
XX
DR WPI; 2003-196707/19.
DR N-PSDB; ABK79229.
XX
XX
PT Antibody for detecting antigen in animal or killing cells carrying
PT antigen comprises human constant region and variable region having
PT specificity for human tumor antigen bound by ING-1 antibody.
XX
XX
PS Example 3; Fig 14; 101pp; English.
XX
CC The invention describes an antibody comprising a human constant region
CC and a variable region having specificity for the human tumour antigen
CC bound by the ING-1 antibody, where the ING-1 is produced by cell line
CC HB912 as deposited with ATCC, and the antibody has the same affinity as
CC the ING-1 for the human tumour antigen. The antibody is useful in an
CC immunoassay method for detecting an antigen in a sample by contacting a
CC label-detectable antigen in the sample with the antibody, detecting the
CC label and relating the detected label to the presence of the antigen; for
CC use in an imaging method for revealing the presence of a label-detectable
CC antigen in an animal by contacting the antibody with a part of the animal
CC suspected of containing the antigen, detecting the label and relating the
CC detected label to the presence of the antigen; and for killing cells
CC carrying an antigen by contacting the cells with the antibody and
CC allowing the killing to occur. The antibodies are useful in tumour
CC diagnosis and therapy. The chimeric antibodies bind to the surface of
CC human tumour cells but do not bind detectably to normal cells, e.g.,
CC fibroblasts, endothelial cells or epithelial cells in the major organs.
CC The high biological activity of the chimeric antibodies against human
CC tumour cell lines combined with minimal reactivity with normal tissues
CC imply that these antibodies may mediate selective destruction of
CC malignant tissue. The presence of human rather than murine antigenic
CC determinants on the chimeric antibodies increases their resistance to
CC rapid clearance from the body relative to the original murine mabs. This
CC resistance to clearance enhances the potential utility of these chimeric
CC antibodies, as well as their derivatives, in tumour diagnosis and
CC therapy. This is the amino acid sequence of a mouse antibody light chain
CC variable region used in the creation of an anti-human tumour antigen-
CC antibody

SQL Sequence 131 AA;
Query Match 96.4%; Score 553; DB 6; Length 131;
Best Local Similarity 96.4%; Pred. No. 3.2e-39;
Matches 106; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 QAVVTQSSALTTSPGETVTLTCRSSSTGAVTTSNANVQEKPDHLPFTGLIGGTINRVGV 60
DB 20 QAVVTQSSALTTSPGETVTLTCRSSSTGAVTTSNANVQEKPDHLPFTGLIGGTINRVAGV 79
QY 61 PARPSSGLIGDKKALTTTGAQTEDEALYFCALWYSNHWVFGGRTKLTVLG 110
DB 80 PARPSSGLIGDKKALTTTGTDEALYFCALWYSNHWVFGGRTKLTVLG 129
RESULT 9
ADM07541
ID ADM07541 standard; protein; 114 AA.
XX
AC ADM07541;
XX
DT 20-MAY-2004 (first entry)
XX
DE Murine immunoglobulin 15A2 light chain variable domain protein.
XX
KM murine; mouse; heavy; immunoglobulin;
KM antibody light chain variable domain; antiallergic; allergy; IgE;
KM gene therapy; 15A2.
XX
OS Mus sp.
XX
PN WO2003060080-A2.
XX
PD 24-JUL-2003.
XX
PF 20-DEC-2002; 2002MO-US041362.
XX
PR 21-DEC-2001; 2001US-0344874P.
XX
PA (IDEXX -) IDEXX LAB INC.
XX
PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX
DR WPI; 2003-598521/56.
XX
XX
PT New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
PS Example 5; Fig 2; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a murine
CC immunoglobulin light chain variable domain protein of the invention.
XX
SQ Sequence 114 AA;
Query Match 96.0%; Score 553; DB 7; Length 114;
Best Local Similarity 96.4%; Pred. No. 4e-39;
Matches 106; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 QAVVTQSSALTTSPGETVTLTCRSSSTGAVTTSNANVQEKPDHLPFTGLIGGTINRVGV 60
DB 4 QAVVTQSSALTTSPGETVTLTCRSSSTGAVTTSNANVQEKPDHLPFTGLIGGTINRVAGV 63
QY 61 PARPSSGLIGDKKALTTTGAQTEDEALYFCALWYSNHWVFGGRTKLTVLG 110
DB 64 PARPSSGLIGDKKALTTTGAQTEDEALYFCALWYSNHWVFGGRTKLTVLG 113
RESULT 10
AAR95949

ID AAR5949 standard; protein; 128 AA.
 AC AAR5949;
 XX
 DT 11-FEB-1997 (first entry)
 XX
 DE 3G3 variable lambda chain.
 XX
 KM Antibody; HNK-20; variable heavy chain; hybridoma; murine; IgA; mouse;
 KW F glycoprotein; respiratory syncytial virus; RSV; constant region gene;
 KW chimeric antibody; isotype-switched antibody; therapy; infection; human;
 KW pneumonia; bronchiolitis; animal.
 XX
 OS Mus musculus.
 XX
 PN WO9616974-A1.
 XX
 PD 06-JUN-1996.
 XX
 PF 01-DEC-1995; 95WO-US015716.
 XX
 PR 01-DEC-1994; 94US-00348548.
 XX
 PA (ORAV-) ORAVAX INC.
 XX
 PI Berdoz J, Kraehenbuhl J;
 XX
 DR WPI; 1996-286826/29.
 DR N-PSDB; AAT30559.
 XX
 PT DNA encoding variable region of antibody HNK-20 - for treating
 PT respiratory syncytial virus infection.
 XX
 PS Example; Page 29; 75pp; English.
 XX
 CC This sequence represents the variable lambda chain of an antibody
 CC produced by the 3G3 hybridoma cell line. AAR5949-R5948 represent
 CC sequences for variable regions of an antibody produced by the hybridoma
 CC cell line HNK-20. HNK-20 and 3G3 are murine hybridoma cell lines, that
 CC produces IgA specific for the F glycoprotein of respiratory syncytial
 CC virus (RSV). The DNA encoding these sequences were isolated using primers
 CC specific for the 5' untranslated region of the variable region, and for
 CC the intron downstream of the rearranged J region (see AAT30459-T30545 for
 CC primer sequences). The DNA encoding these sequences can be inserted into
 CC vectors containing heterologous (such as human) constant region genes,
 CC for the production of chimeric and isotype-switched antibodies. The
 CC antibodies are useful in the treatment and diagnosis of infection by RSV,
 CC such as pneumonia and bronchiolitis, in humans and animals. By using
 CC genomic DNA as a template, variable region genes can be isolated without
 CC producing fragments that have to be adapted for recombinant antibody
 CC expression. Also, by using the genomic DNA, no knowledge of the DNA
 CC sequence encoding the target variable region is required. Chimeric
 CC antibodies produced from these proteins, that contain the constant region
 CC of the host being treated, are less likely to cause adverse immune
 CC reactions
 XX
 SQ Sequence 128 AA;
 Query Match 96.0%; Score 553; DB 2; Length 128;
 Best Local Similarity 97.2%; Pred. No. 4.6e-39;
 Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QAVTQSSALTTSGEVTTLTCRSSGAVTTSNANWQEKPDHFTGLIGTINRVPV 60
 DB 20 QAVTQSSALTTSGEVTTLTCRSSGAVTTSNANWQEKPDHFTGLIGTINRPA 79
 QY PARFSSGLIGDKAALTTTGAQTEDEAIFYCALMYSNHWVFGGGLTLYL 109
 DB 80 PARFSSGLIGDKAALTTTGAQTEDEAIFYCALMYSNHWVFGGGLTLYL 128

RESULT 11
 AAY03868

ID AAY03868 standard; protein; 112 AA.
 XX
 AC AAY03868;
 XX
 DT 16-JUN-1999 (first entry)
 XX
 DE SM3 light chain variable region.
 XX
 KM SM3 antibody; epitope; mimic; crystal; tumour; MUC1 epitope; allergy;
 KW immune response; arthritis; multiple sclerosis; asthma; diabetes;
 KW inflammatory disorder; transplant rejection; graft versus host disease.
 XX
 OS Unidentified.
 XX
 PN WO9910379-A1.
 XX
 PD 04-MAR-1999.
 XX
 PF 24-AUG-1998; 98WO-GB002542.
 XX
 PR 22-AUG-1997; 97GB-00017946.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 XX
 PI Freemont PS, Snary D, Sternberg ME, Bates PA, Dokurno P;
 XX
 DR WPI; 1999-204650/17.
 DR N-PSDB; AAX31970.
 XX
 PT New SM3 antibody crystal structures - used to develop agents for treating
 PT e.g. tumour, autoimmune disorders, allergies, inflammatory disorders or
 PT transplant rejection.
 XX
 PS Disclosure; Page 279; 316pp; English.
 XX
 CC The invention relates to a process for preparing a crystal using cadmium.
 CC Structure factors or structural coordinates obtained from the crystal of
 CC SM3 antibody bound to an epitope can be used to design mimics of the
 CC antibody or the epitope. The crystals comprise at least an epitope
 CC binding fragment of the SM3 antibody bound to a peptide recognised by the
 CC epitope binding site of SM3. The products and methods can be used to
 CC develop agents for the detection of tumour cells and for therapy against
 CC tumours. MUC1 epitope mimics can also be used to prevent or decrease an
 CC immune response, e.g. in the therapy of diseases caused by autoimmune
 CC responses (such as arthritis, multiple sclerosis, asthma or diabetes),
 CC allergies, inflammatory disorders or transplant rejections such as graft
 CC versus host disease. The present sequence represents the amino acid
 CC sequence of a light chain variable region of SM3 antibody
 XX
 SQ Sequence 112 AA;
 Query Match 95.5%; Score 550; DB 2; Length 112;
 Best Local Similarity 97.2%; Pred. No. 7.1e-39;
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 VVTOESALTTSPGETVTLTCRSSGAVTTSNANWQEKPDHFTGLIGTINRVPV 62
 DB 3 VVTOESALTTSPGETVTLTCRSSGAVTTSNANWQEKPDHFTGLIGTINRPA 62
 QY 63 RFSSGLIGDKAALTTTGAQTEDEAIFYCALMYSNHWVFGGGLTLYL 110
 DB 63 RFSSGLIGDKAALTTTGAQTEDEAIFYCALMYSNHWVFGGGLTLYL 110
 RESULT 12
 AAY44990
 ID AAY44990 standard; protein; 261 AA.
 XX
 AC AAY44990;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE Murine anti-Lewis Y antibody single-chain Fv fragment.

XX Murine; Lewis Y; IgY; antibody; single-chain Fv fragment; scFv;
 KW heteromultibody; multifunctional compound; CH1 domain; CL domain;
 KW heavy chain; constant domain; light chain; CD80 molecule; immunoglobulin;
 KW cyclostatic; immunostimulatory; antileukemia; diagnosis;
 KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;
 KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
 XX
 OS Mus sp.
 XX
 FH Key
 FT Region
 FT Region
 FT Region
 FT Region
 XX
 PN WO200006605-A2.
 XX
 PD 10-FEB-2000.
 XX
 PD 28-JUL-1999; 99WO-EP005416.
 XX
 PR 28-JUL-1998; 98EP-00114082.
 XX
 PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
 XX
 PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zetzel F;
 DR WPI; 2000-195265/17.
 DR N-PSDB; AAZ50583.
 XX
 PT New multifunctional compounds useful for preventing and/or treating
 PT malignant cell growth and for detection and diagnosis.
 XX
 PS Claim 8; Fig 6; 166pp; English.
 XX
 CC The patent discloses heteromultibodies which are multifunctional compounds
 CC producible in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises a CH1 domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises CL domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (polypeptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (polypeptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteromultibodies have
 CC cyclostatic, immunostimulatory, antileukemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of hematopoietic
 CC cells e.g. lymphomas and leukemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas. The present sequence is a murine anti-Lewis Y
 CC antibody single-chain Fv (scFv) fragment which is used in the
 CC construction of heteromultibodies comprising CH1 (first constant domain of
 CC human IgG1 heavy chain), CK (constant region of human Ig-kappa light
 CC chain) and CD80 molecule
 XX
 SQ Sequence 261 AA;
 Query Match 95.1%; Score 548; DB 3; Length 261;
 Best Local Similarity 97.2%; Pred. No. 2.6e-38;
 Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 VVTQESALTTSPGETVTITCRSSGTGAVTTSNSANWVOEKPHLFTGLIGGTINRVPVPA 62
 DB 22 VVTQESALTTSPGETVTITCRSSGTGAVTTSNSANWVOEKPHLFTGLIGGTINRVPVPA 81
 QY 63 RFGSGSLIGDKKALTTTGAGTDEDAIYFCALWYSNHWVFGGCTKLTVL 110
 DB 82 RFGSGSLIGDKKALTTTGAGTDEDAIYFCALWYSNHWVFGGCTKLTVL 129

ID ADM07542 standard; protein; 229 AA.
 XX
 AC ADM07542;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Murine immunoglobulin 15A2/1NQG light chain variable domain protein.
 XX
 KW murine; mouse; heavy; immunoglobulin;
 KW antibody light chain variable domain; antiallergic; allergy; IgB;
 KW gene therapy; 15A2/1NQG.
 XX
 OS Mus sp.
 XX
 PN WO2003060080-A2.
 XX
 PD 24-JUL-2003.
 XX
 PD 20-DEC-2002; 2002WO-US041362.
 XX
 PR 21-DEC-2001; 2001US-0344874P.
 XX
 PA (IDEXX-) IDEXX LAB INC.
 XX
 PI Krah ER, Guo H, Aiyappa A, Lawton R;
 DR WPI; 2003-598521/56.
 XX
 PT New canine heavy and light chain variable domain polypeptides, useful for
 PT treating canine allergy.
 XX
 PS Example 6; Fig 5; 130pp; English.
 XX
 CC The invention relates to a novel canine heavy or light chain variable
 CC domain polypeptide. The protein of the invention demonstrates
 CC antiallergic activity and may be useful for treating canine allergy,
 CC possibly via gene therapy. The current sequence is that of a murine
 CC immunoglobulin light chain variable domain protein of the invention.
 CC
 XX
 SQ Sequence 229 AA;
 Query Match 95.0%; Score 547; DB 7; Length 229;
 Best Local Similarity 96.3%; Pred. No. 2.7e-38;
 Matches 105; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QAVVTQESALTTSPGETVTITCRSSGTGAVTTSNSANWVOEKPHLFTGLIGGTINRVPVPA 60
 DB 1 QAVVTQESALTTSPGETVTITCRSSGTGAVTTSNSANWVOEKPHLFTGLIGGTINRVPVPA 60
 QY 61 PARFGSLIGDKKALTTTGAGTDEDAIYFCALWYSNHWVFGGCTKLTVL 109
 DB 61 PARFGSLIGDKKALTTTGAGTDEDAIYFCALWYSNHWVFGGCTKLTVL 109
 RESULT 14
 ID ADM07544 standard; protein; 229 AA.
 XX
 AC ADM07544;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Murine immunoglobulin 15A2/2VIR light chain variable domain protein.
 XX
 KW murine; mouse; heavy; immunoglobulin;
 KW antibody light chain variable domain; antiallergic; allergy; IgB;
 KW gene therapy; 15A2/2VIR.
 XX
 OS Mus sp.
 XX
 PN WO2003060080-A2.
 XX
 PD 24-JUL-2003.

XX 20-DEC-2002; 2002MO-US041362.
 PF
 XX
 PR 21-DEC-2001; 2001US-0344874P.
 XX
 PA (IDEX-) IDEXX LAB INC.
 XX
 PI Krah ER, Guo H, Aiyappa A, Lawton R;
 XX WPI; 2003-598521/56.
 DR
 XX
 PT New canine heavy and light chain variable domain polypeptides, useful for
 PT treating canine allergy.
 XX
 PS Example 6; Fig 5; 130pp; English.
 XX
 CC The invention relates to a novel canine heavy or light chain variable
 CC domain polypeptide. The protein of the invention demonstrates
 CC antiallergic activity and may be useful for treating canine allergy,
 CC possibly via gene therapy. The current sequence is that of a murine
 CC immunoglobulin light chain variable domain protein of the invention.
 CC
 SQ Sequence 229 AA;

Query Match 95.0%; Score 547; DB 7; Length 229;
 Best Local Similarity 96.3%; Pred. No. 2.7e-38;
 Matches 105; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGETVTLTCRSSTGAVTTSNANWVQEKPDHLEFTGLIGGTINRVPGV 60
 DB 1 QAVVTOESALTTSPGETVTLTCRSSTGAVTTSNANWVQEKPDHLEFTGLIGGTINRVPGV 60
 QY 61 PARFSGSLIGDKAALTTTGAQTEDEDAIYFCALWYSNHWVFGGXTLTVL 109
 DB 61 PARFSGSLIGDKAALTTTGAQTEDEDAIYFCALWYSNHWVFGGXTLTVL 109

RESULT 15

ADM07543
 ID ADM07543 standard; protein; 230 AA.

AC ADM07543;

DT 20-MAY-2004 (first entry)

DE Murine immunoglobulin 15A2/1FBI light chain variable domain protein.

XX murine; mouse; heavy; immunoglobulin;
 KW antibody light chain variable domain; antiallergic; allergy; IGE;
 KW gene therapy; 15A2/1FBI.

XX Mus sp.

XX WO2003060080-A2.

XX 24-JUL-2003.

XX 20-DEC-2002; 2002MO-US041362.

XX 21-DEC-2001; 2001US-0344874P.

XX (IDEX-) IDEXX LAB INC.

XX Krah ER, Guo H, Aiyappa A, Lawton R;

XX WPI; 2003-598521/56.

XX New canine heavy and light chain variable domain polypeptides, useful for
 PT treating canine allergy.

XX Example 6; Fig 5; 130pp; English.

XX The invention relates to a novel canine heavy or light chain variable

CC domain polypeptide. The protein of the invention demonstrates
 CC antiallergic activity and may be useful for treating canine allergy,
 CC possibly via gene therapy. The current sequence is that of a murine
 CC immunoglobulin light chain variable domain protein of the invention.
 CC
 SQ Sequence 230 AA;

Query Match 95.0%; Score 547; DB 7; Length 230;
 Best Local Similarity 96.3%; Pred. No. 2.7e-38;
 Matches 105; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGETVTLTCRSSTGAVTTSNANWVQEKPDHLEFTGLIGGTINRVPGV 60
 DB 2 QAVVTOESALTTSPGETVTLTCRSSTGAVTTSNANWVQEKPDHLEFTGLIGGTINRVPGV 61
 QY 61 PARFSGSLIGDKAALTTTGAQTEDEDAIYFCALWYSNHWVFGGXTLTVL 109
 DB 62 PARFSGSLIGDKAALTTTGAQTEDEDAIYFCALWYSNHWVFGGXTLTVL 110

Search completed: December 29, 2004, 17:57:32
 Job time : 78.6047 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:38:43 / Search time 75.992 Seconds
(without alignments)
833.556 Million cell updates/sec

Title: US-10-774-076-5

Perfect score: 576

Sequence: 1 QAVYQESALTTSPGETVTL.....ALWYSHHWFGGKTLTVLG 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of residues predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	552	95.8	129 1	LVID_MOUSE
2	552	95.8	129 1	LVID_MOUSE
3	551	95.7	129 1	LVID_MOUSE
4	540	93.8	129 2	Q8VDE2
5	535.5	93.0	113 2	Q8CGS1
6	534	92.7	110 1	LVID_MOUSE
7	530.5	92.1	109 2	Q9ETI3
8	514	89.2	129 1	LVID_MOUSE
9	487	84.5	117 1	LVID_MOUSE
10	460	79.9	117 1	LVID_MOUSE
11	279	48.4	117 1	LVID_MOUSE
12	244.5	42.4	111 1	LVID_MOUSE
13	239.5	41.6	107 2	Q9NSD6
14	239	41.5	236 2	Q6GMV7
15	236.5	41.1	111 1	LVID_MOUSE
16	236.5	41.1	237 2	Q8WUK4
17	235.5	40.9	237 2	Q8WUK4
18	234	40.6	110 2	LVID_MOUSE
19	234	40.6	112 1	LVID_MOUSE
20	233.5	40.5	233 2	Q8NSF4
21	233.5	40.5	248 2	Q7SYU1
22	233	40.5	112 1	LVID_MOUSE
23	232	40.3	236 2	Q6GMV7
24	231.5	40.2	130 1	LVID_MOUSE
25	228.5	39.7	109 1	LVID_MOUSE
26	228	39.6	233 2	Q6PJ33
27	228	39.6	233 2	AAR18749
28	227.5	38.5	108 1	LVID_MOUSE
29	227.5	38.5	111 1	LVID_MOUSE
30	227.5	38.5	116 2	Q6GJDO
31	227	39.4	236 2	Q6IPQ0

32	226.5	39.3	167 2	BAC05245	BAC05245 homo sapi
33	226.5	39.3	235 2	Q6GMV6	Q6GMV6 homo sapien
34	226	39.2	236 2	Q8NEJ1	Q8NEJ1 homo sapien
35	225.5	39.1	235 2	Q6PIK1	Q6PIK1 homo sapien
36	225.5	39.1	235 2	AAR33102	AAR33102 homo sapi
37	223	38.7	230 2	Q722U3	Q722U3 homo sapien
38	223	38.7	236 2	Q9GEB1	Q9GEB1 homo sapien
39	222.5	38.6	245 2	Q6GNC5	Q6GNC5 xenopus lae
40	222	38.5	236 2	Q6PIQ7	Q6PIQ7 homo sapien
41	222	38.5	236 2	AAR30983	AAR30983 homo sapi
42	221.5	38.5	111 1	LVID_MOUSE	P80422 homo sapien
43	220.5	38.3	111 1	LVID_MOUSE	P80422 homo sapien
44	220.5	38.3	235 2	BAC85358	BAC85358 homo sapi
45	219.5	38.1	233 2	Q8TBC9	Q8TBC9 homo sapien

ALIGNMENTS

RESULT 1				
ID	LVID_MOUSE	STANDARD;	PRT;	129 AA.
AC	P01726;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Ig lambda-1 chain V region H2020 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
ON	NCBI_TaxId=10090;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RK	MEDLINE=79084170; PubMed=103630;			
RA	Bernard O., Hozumi N., Tonegawa S.;			
RT	"Sequences of mouse immunoglobulin light chain genes before and after			
RT	somatic changes."			
RL	Cell 15:1133-1144(1978).			
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	HSP; P01724; IABV.			
DR	InterPro; IPR007110; Ig_1like.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV_1.			
DR	PROSITE; PS50835; Ig_Like; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL 1			
FT	CHAIN 20 129			
FT	DOMAIN 20 125			
FT	NON_TER 129 129			
SQ	SEQUENCE 129 AA; 13465 MW; A57C8910157C1316 CRC64;			
Query Match				
Best Local Similarity 95.8%; Score 552; DB 1; Length 129;				
Matches 105; Conservative 1; Mismatches 4; Indels 0; Gaps 0;				
QY	1 QAVYQESALTTSPGETVTLTCRSSTGAVTTSNSANWYQERPDHIFTLIGGTTNRVGV 60			
DB	20 QAVYQESALTTSPGETVTLTCRSSTGAVTTSNSANWYQERPDHIFTLIGGTTNRVGV 79			
QY	61 PARFSGSLIGKALTTGAQTDEATYFCALWYSHHWFGGKTLTVLG 110			
DB	80 PARFSGSLIGKALTTGAQTDEATYFCALWYSHHWFGGKTLTVLG 129			
RESULT 2				
ID	LVID_MOUSE	STANDARD;	PRT;	129 AA.
AC	P01727;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Ig lambda-1 chain V region S43 precursor.			

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82220143; PubMed=6283385;
 RA Botwell A.L.M., Paskind M., Reih M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Somatic variants of murine immunoglobulin lambda light chains.";
 RL Nature 298:380-382(1982).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP; P01724; 1A6V.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT CHAIN 1 19
 FT DOMAIN 20 129 Ig lambda-1 chain V region S43.
 FT NON_TER 129 IG-like.
 FT SEQUENCE 129 AA; 13529 MW; 84B54E7D5791345 CRC64;
 SQ

Query Match 95.8%; Score 552; DB 1; Length 129;
 Best Local Similarity 95.5%; Pred No. 1.4e-46;
 Matches 105; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 QAVVTQESALTTSPETVTLTCRSSTGAVTTSNSANWVOEKPDHFTGLIGTINRVGV 60
 DB 20 QAVVTQESALTTSPETVTLTCRSSTGAVTTSNSANWVOEKPDHFTGLIGTINRVAGV 79
 OY 61 PARFSGSLIGDKAALTTGAQTEDEAIFYCALWYSNHWVFGGTRKLTVLG 110
 DB 80 PARFSGSLIGDKAALTTGAQTEDEAIFYCALWYSNHWVFGGTRKLTVLG 129

RESULT 3
 LVLB MOUSE STANDARD; PRT; 129 AA.
 AC P01724;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-29 (MOPC 104E), AND REVISIONS TO 20 AND 26.
 RX MEDLINE=71148916; PubMed=403522;
 RA Bursstein Y., Schechter I.;
 RT "Amino acid sequence of the NH2-terminal extra piece segments of the
 RT precursors of mouse immunoglobulin lambda1-type and kappa-type light
 RT chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
 RN [2]
 RP SEQUENCE OF 20-129 (MOPC 104E AND RPC 20).
 RX MEDLINE=71107854; PubMed=5276767;
 RA Appella E.;
 RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
 RN [3]
 RP REVISIONS (MOPC 104E).
 RX MEDLINE=73229669; PubMed=4516208;
 RA Appella E.;
 RL Unpublished results, cited by;
 RL Cesari I.M., Weigert M.;
 RL Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
 RN [4]
 RP SEQUENCE OF 20-129 (J558 AND S104).

RX MEDLINE=73229669; PubMed=4516208;
 RA Cesari I.M., Weigert M.;
 RT "Mouse lambda-chain sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
 CC -1- MISCELLANEOUS: Compositions and partial sequences of RPC 20 show
 CC no differences from MOPC 104E. The sequences of J558 and S104
 CC seems identical with that shown.
 CC -1- MISCELLANEOUS: These proteins were isolated from serum or urine of
 CC tumor-bearing mice.
 CC -1- MISCELLANEOUS: The MOPC 104E precursor was synthesized in a cell-
 CC free system directed by mRNA isolated from MOPC 104E myeloma
 CC polyomes. Met-1 was lacking in 90% of the chains. It is probably
 CC rapidly cleaved after synthesis.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; B93815; LIMS4E.
 DR PDB; 1A6U; X-ray; L=21-128.
 DR PDB; 1A6V; X-ray; L/M/N=20-129.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR 3D-structure; Direct protein sequencing; Immunoglobulin V region;
 KW Pyroglutamate carboxylic acid; Signal.
 FT CHAIN 1 19
 FT SIGNAL 20 129
 FT DOMAIN 20 125
 FT MOD_RBS 20 20
 FT STRAND 23 25
 FT STRAND 28 31
 FT TURN 33 34
 FT STRAND 36 43
 FT TURN 44 45
 FT STRAND 46 46
 FT TURN 50 52
 FT HELIX 55 60
 FT STRAND 61 63
 FT TURN 64 70
 FT STRAND 71 73
 FT STRAND 74 75
 FT TURN 77 78
 FT TURN 81 82
 FT STRAND 83 88
 FT TURN 89 90
 FT STRAND 91 97
 FT STRAND 101 103
 FT HELIX 105 112
 FT STRAND 117 119
 FT STRAND 123 127
 FT NON_TER 129 129
 FT SEQUENCE 129 AA; 13479 MW; 03629939D5791AC0 CRC64;
 SQ

Query Match 95.7%; Score 551; DB 1; Length 129;
 Best Local Similarity 95.5%; Pred No. 1.8e-46;
 Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 QAVVTQESALTTSPETVTLTCRSSTGAVTTSNSANWVOEKPDHFTGLIGTINRVGV 60
 DB 20 QAVVTQESALTTSPETVTLTCRSSTGAVTTSNSANWVOEKPDHFTGLIGTINRVAGV 79
 OY 61 PARFSGSLIGDKAALTTGAQTEDEAIFYCALWYSNHWVFGGTRKLTVLG 110
 DB 80 PARFSGSLIGDKAALTTGAQTEDEAIFYCALWYSNHWVFGGTRKLTVLG 129

RESULT 4
 O8VDE2 PRELIMINARY; PRT; 129 AA.
 AC O8VDE2;
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE Immunoglobulin lambda chain variable region (Fragment).
GN Name=4612-A-H10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Welle G.;
RL Theis (1995), Department of Ecole Supérieure de Technicien en
Biologie Biochimie, Université Catholique de Lyon, Lyon, France.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Blachere T.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR HSSP; P01724; 1A6V.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 129
SQ SEQUENCE 129 AA; 13565 MW; C07F71003803ADB CRC64;

Query Match 93.8%; Score 540; DB 2; Length 129;
Best Local Similarity 93.6%; Pred. No. 2,2e-45;
Matches 103; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPETVTLTCRSSTGAVTTSNSANWQEKPDHLPGLIGGINRVGV 60
DB 20 QAVTQESALTTSPETVTLTCRSSTGAVTTSNSANWQEKPDHLPGLIGGINRVGV 79
QY 61 PARFSGSLIGDKALTTTGAQTEDEAIFCALWYSNHWVFGGKTLTVLG 110
DB 80 PARFSGSLIGDKALTTTGAQTEDEAIFCALWYSNHWVFGGKTLTVLG 129

RESULT 5
O8CGS1 PRELIMINARY; PRT; 113 AA.
AC O8CGS1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-deoxyribovalenol scFv lambda light chain variable region
DS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Wang Z., Munshi K., Osawa F., Pestka J.J., Hart L.P.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY151141; AAN75453.1;
DR HSSP; P01724; 1A6V.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12034 MW; 0C4E4C65597E22BE CRC64;

Query Match 93.0%; Score 535.5; DB 2; Length 113;
Best Local Similarity 94.6%; Pred. No. 5,3e-45;

Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 QAVTQESALTTSPETVTLTCRSSTGAVTTSNSANWQEKPDHLPGLIGGINRVGV 60
DB 1 QAVTQESALTTSPETVTLTCRSSTGAVTTSNSANWQEKPDHLPGLIGGINRVGV 60
QY 61 PARFSGSLIGDKALTTTGAQTEDEAIFCALWYSNHWVFGGKTLTVLG 110
DB 61 PARFSGSLIGDKALTTTGAQTEDEAIFCALWYSNHWVFGGKTLTVLG 111

RESULT 6
LVIC MOUSE
ID LVIC MOUSE STANDARD; PRT; 110 AA.
AC P01725;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda-1 chain V region S178.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=73229669; PubMed=4516208;
RA Ceasari I.M., Weigert M.;
RT "Mouse lambda-chain sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
CC -1- MISCELLANEOUS: This protein was isolated from serum or urine of
-1- tumor-bearing mice.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01724; 1A6V.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 106
FT NON_TER 110
FT NON_TER 110
SQ SEQUENCE 110 AA; 11654 MW; 7D06718B1A530206 CRC64;

Query Match 92.7%; Score 534; DB 1; Length 110;
Best Local Similarity 92.7%; Pred. No. 7,2e-45;
Matches 102; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPETVTLTCRSSTGAVTTSNSANWQEKPDHLPGLIGGINRVGV 60
DB 1 QAVTQESALTTSPETVTLTCRSSTGAVTTSNSANWQEKPDHLPGLIGGINRVGV 60
QY 61 PARFSGSLIGDKALTTTGAQTEDEAIFCALWYSNHWVFGGKTLTVLG 110
DB 61 PARFSGSLIGDKALTTTGAQTEDEAIFCALWYSNHWVFGGKTLTVLG 110

RESULT 7
Q9ETI3 PRELIMINARY; PRT; 109 AA.
ID Q9ETI3
AC Q9ETI3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Song M.-Y., Kang H.-K., Kwag W.-J., Moon H.-J., Song T.-H., Ko I.-Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF287275; AAC03053.1; -
 DR HSP; P01724; 1A6V.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1 109
 FT SIGNAL 109 109
 SQ SEQUENCE 109 AA; 11554 MW; 4F91E9D351B1E158 CRC64;
 Query Match 92.1%; Score 530.5; DB 2; Length 109;
 Best Local Similarity 93.6%; Pred. No. 1.6e-44;
 Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
 QY 1 QAVVDESALTTPGRTVTLTCRSSGTGAVTTSNSANWVOEKPDHFTGLIGGTINRPGV 60
 DB 1 QAVVDESALTTPGRTVTLTCRSSGTGAVTTSNSANWVOEKPDHFTGLIGGTINRPGV 60
 QY 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNHWVFGGGLTVLG 110
 DB 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMY-SNNVFGGGLTVLG 109
 RESULT 8
 LV2B_MOUSE STANDARD; PRT; 129 AA.
 AC P01729;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig lambda-2 chain V region MOPC 315 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82274221; PubMed=6287422;
 RA Wu G.E., Govindji N., Hozumi N., Murialdo H.;
 RT "Nucleotide sequence of a chromosomal rearranged lambda 2
 immunoglobulin gene of mouse.";
 RL Nucleic Acids Res. 10:3831-3843 (1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82220143; PubMed=6283385;
 RA Boehmell A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RT Baltimore D.;
 RL "Somatic variants of murine immunoglobulin lambda light chains.";
 RN Nature 298:380-382 (1982).
 RN [3]
 RP SEQUENCE OF 1-22.
 RX MEDLINE=79148758; PubMed=428562;
 RA Schechter I., Wolf O., Zemell R., Burstein Y.;
 RT "Structure and function of immunoglobulin genes and precursors.";
 RL Fed. Proc. 38:1839-1845 (1979).
 RN [4]
 RP SEQUENCE OF 20-129.
 RX MEDLINE=7404693; PubMed=4760498;
 RA Dugan B.S., Bradshaw R.A., Simms E.S., Eisen H.N.;
 RT "Amino acid sequence of the light chain of a mouse myeloma protein
 (MOPC-315).";
 RL Biochemistry 12:5400-5416 (1973).
 RN [5]
 RP DETERMINATION OF AMIDATION STATES OF 58; 59; 62; 100; 102 AND 115.
 RX MEDLINE=78187254; PubMed=418602;
 RA Gavish M., Zakut R., Wilchek M., Givol D.;
 RT "Preparation of a semisynthetic antibody.";
 RL Biochemistry 17:1345-1351 (1978).
 CC -1- MISCELLANEOUS: This chain is from a myeloma protein with anti-DNP
 activity.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A93431; L2WS35.

DR HSP; P01724; 1A6V.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region;
 KW Pyrolydione carboxylic acid; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 129
 FT DOMAIN 20 125
 FT MOD_RES 20 20
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 13418 MW; 0AA6E8125723552C CRC64;
 Query Match 89.2%; Score 514; DB 1; Length 129;
 Best Local Similarity 88.2%; Pred. No. 8e-43;
 Matches 97; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 QAVVDESALTTPGRTVTLTCRSSGTGAVTTSNSANWVOEKPDHFTGLIGGTINRPGV 60
 DB 20 QAVVDESALTTPGRTVTLTCRSSGTGAVTTSNSANWVOEKPDHFTGLIGGTINRPGV 79
 QY 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNHWVFGGGLTVLG 110
 DB 80 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMY-SNNVFGGGLTVLG 129
 RESULT 9
 LV1A_MOUSE STANDARD; PRT; 117 AA.
 AC P01723;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-2004 (Rel. 45, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig lambda-1 chain V region precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=79084170; PubMed=103630;
 RA Bernard O., Hozumi N., Tonegawa S.;
 RT "Sequences of mouse immunoglobulin light chain genes before and after
 somatic changes.";
 RL Cell 15:1133-1144 (1978).
 RN [2]
 RP -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; V00811; CAA24193.1; -
 DR PIR; A01994; L1MSV.
 DR HSP; P01724; 1A6V.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 117
 FT DOMAIN 21 117
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12222 MW; 36F3C5601C54B55A CRC64;
 Query Match 84.5%; Score 487; DB 1; Length 117;

Best Local Similarity 96.9%; Pred. No. 3.3e-40;
Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGTYVTLTCSRSTGAVTTSNANWQEKPDHFLFTGLIGTINRPGV 60
DB 21 QAVTQESALTTSPGTYVTLTCSRSTGAVTTSNANWQEKPDHFLFTGLIGTINRPGV 80
QY 61 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALMYSNH 97
DB 81 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALMYSNH 117

RESULT 10

LV2A_MOUSE STANDARD; PRT; 117 AA.

AC P01728; (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig lambda-2 chain V region precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=78179064; PubMed=418414;
RA Torigawa S., Maxam A.M., Tizard R., Bernard O., Gilbert W.;
RT "Sequence of a mouse germ-line gene for a variable region of an
immunoglobulin light chain."
RL Proc. Natl. Acad. Sci. U.S.A. 75:1485-1489(1978).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
CC or send an email to license@isb-sdb.ch).

CC EMBL; J00599; AAA39167.1; -
DR EMBL; V00815; CAA24196.2; -
DR EMBL; X58412; CAA41313.1; -
DR EMBL; X58418; CAA41318.1; -
DR EMBL; X58423; CAA41323.1; -
DR EMBL; X58424; CAA41324.1; -
DR PIR; A01996; L2MSGW.
DR HSSP; P01724; IACV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig lambda-2 chain V region.
FT DOMAIN 20 >117 Ig-like.
FT NON TER 117
SQ SEQUENCE 117 AA; 12222 MW; 43FDF197419842A6 CRC64;

Query Match 79.9%; Score 460; DB 1; Length 117;
Best Local Similarity 89.8%; Pred. No. 1.5e-37;
Matches 88; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGTYVTLTCSRSTGAVTTSNANWQEKPDHFLFTGLIGTINRPGV 60
DB 20 QAVTQESALTTSPGTYVTLTCSRSTGAVTTSNANWQEKPDHFLFTGLIGTINRPGV 79
QY 61 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALMYSNH 98
DB 80 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALMYSNH 117

RESULT 11

LV0A_HUMAN STANDARD; PRT; 117 AA.

AC P04211;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 36, Last annotation update)
DE Ig lambda chain V region 4A precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=85014122; PubMed=6091030;
RA Anderson M.L.M., Szafranc M.F., Kaplan J.C., McCoil L., Young B.D.;
RT "The isolation of a human Ig V lambda gene from a recombinant library
of chromosome 22 and estimation of its copy number."
RL Nucleic Acids Res. 12:6647-6661(1984).
DR PIR; A01993; LVH02.
DR HSSP; P01724; IACV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 117 Ig lambda chain V region 4A.
FT DOMAIN 21 42 Framework-1.
FT DOMAIN 43 55 Complementarity-determining-1.
FT DOMAIN 56 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 117 Complementarity-determining-3.
FT DISULFID 42 110 By similarity.
FT NON TER 117
SQ SEQUENCE 117 AA; 12380 MW; C587B0047CC1CD62 CRC64;

Query Match 48.4%; Score 279; DB 1; Length 117;
Best Local Similarity 60.6%; Pred. No. 1.1e-19;
Matches 57; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGTYVTLTCSRSTGAVTTSNANWQEKPDHFLFTGLIGTINRPGV 60
DB 21 QAVTQESALTTSPGTYVTLTCSRSTGAVTTSNANWQEKPDHFLFTGLIGTINRPGV 80
QY 61 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALMY 94
DB 81 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALMY 114

RESULT 12

LV6C_HUMAN STANDARD; PRT; 111 AA.

AC P06317;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig lambda chain V-VI region SUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=85014122; PubMed=6091030;
RA Solomon A., Kyle R.A., Frangione B.;
RT "Light chain variable region subgroups of monoclonal immunoglobulins
in amyloidosis AL.";

RL (in) Glenner G.G., Oseman E.F., Benditt E.P., Calkins E.,
 RL Cohen A.S., Zucker-Franklin D. (eds.), Plenum Press, New York (1986).
 RL Amyloidosis, pp.449-462, Plenum Press, New York (1986).
 DR PIR; A01988; L6HUST.
 DR PDB; 1CD0; X-ray; A/B=1-111.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 DR 3D-structure; Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 22
 FT DOMAIN 1. Framework-1.
 FT DOMAIN 23 35 Complementarity-determining-1.
 FT DOMAIN 36 50 Framework-2.
 FT DOMAIN 51 57 Complementarity-determining-2.
 FT DOMAIN 58 91 Framework-3.
 FT DOMAIN 92 100 Complementarity-determining-3.
 FT DOMAIN 101 111 Framework-4.
 FT DISULFID 22 91 By similarity.
 FT STRAND 4 5
 FT STRAND 9 12
 FT TURN 14 15
 FT STRAND 18 24
 FT HELIX 29 31
 FT STRAND 35 39
 FT TURN 41 42
 FT STRAND 46 50
 FT TURN 51 53
 FT STRAND 54 54
 FT TURN 57 58
 FT TURN 61 62
 FT STRAND 63 68
 FT TURN 69 72
 FT STRAND 73 78
 FT HELIX 83 85
 FT STRAND 87 95
 FT TURN 96 97
 FT STRAND 98 102
 FT STRAND 105 109
 FT NON TER 111
 SQ SEQUENCE 111 AA; 12247 MW; 0941DD547D983598 CRC64;
 Query Match 42.4%; Score 244.5; DB 1; Length 111;
 Best Local Similarity 46.4%; Pred. No. 2.6e-16;
 Matches 51; Conservative 19; Mismatches 37; Indels 3; Gaps 2;
 QY 3 VTQESALITSPGGEVTLTCRSTGAVTTSNSAMVQEKPDHPTGLIGTINRVPGPVPA 62
 DB 3 MLTQPHSVSESPKTVIISCRSDGTI-AGTYVWYQORFERAPFTVIFEDTORPSGVPD 61
 QY 63 FSGSL--IGDKALITTTGAQTEDEAIYFCALWYSNMWVFGGKLTVLG 110
 DB 62 RFGSSIDRSSNSASLTISGLQTEDEADYCYGSDYRDHNVFGGKLTVLG 111
 RESULT 13
 QNSND6 PRELIMINARY; PRT; 107 AA.
 AC QNSND6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Homo sapiens This CDS feature is included to show the translation of
 DE the corresponding V region. Presently translation qualifiers on
 DE V region features are illegal. (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocyte;
 RA Hohmann A.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L43092; AAA69746.2; -.
 DR PIR; S70444; S70444.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 FT NON TER 1
 FT NON TER 107
 SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;
 Query Match 41.6%; Score 239.5; DB 2; Length 107;
 Best Local Similarity 50.5%; Pred. No. 7.7e-16;
 Matches 55; Conservative 15; Mismatches 34; Indels 5; Gaps 2;
 QY 4 VTQESALITSPGGEVTLTCRSTGAVTTSNSAMVQEKPDHPTGLIGTINRVPGPVPA 63
 DB 2 LTQDPVSVVALGGTVITTC--GDSLRSYASWYQKQKQAPVLYYKNNRPSGIDPR 58
 QY 64 FSGSLIGDKALITTTGAQTEDEAIYFCALWYS--NMWVFGGKLTVLG 110
 DB 59 FSGSSSGNTASTLTITGAQAEDEADYCNRSRDSGNHAFVGGKLTVLG 107
 RESULT 14
 QNSND6 PRELIMINARY; PRT; 236 AA.
 AC QNSND6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matsushita K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.,
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073795; AAH73795.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig CL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.

DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 24950 MW; 3B0477247847E930 CRC64;

Query Match 41.5%; Score 239; DB 2; Length 111;
Best Local Similarity 46.0%; Pred. No. 2.1e-15;
Matches 52; Conservative 20; Mismatches 37; Indels 4; Gaps 2;

OY 1 QAVVQESALTTSPGRTVLTFCRSSTGAVTNSANWVQEKPDHFTGLIGGTINRPGV 60
DB 20 QSVLTQPSVSGTSGQRTVITSCGSSSN-GANNVWYQQLPGTAPKLIHTTNQPSGV 78
OY 61 PARFGSLIGDKALTTGAQTEDBAIYFCAIM--YSNHWVFGGKTLTVLG 110
DB 79 PERFGSKSGPSASLVISGLQSEDEAFYCAAMDSDLGPPYFGTGKTVTVLG 131

RESULT 15

LV2C_HUMAN STANDARD; PRT; 111 AA.
ID LV2C_HUMAN
AC P01706
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG lambda chain V-II region BOH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=7515478; PubMed=804002;
RA Kohler H., Rudofsky S., Klusens L.;
RT "The primary structure of a human lambda II chain.";
RL J. Immunol. 114:415-421(1975).
CC -1- MISCELLANEOUS: The C region of this chain has the O2+ marker.
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01972; L2HTBH.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolytic carboxylic acid.
FT DOMAIN 1 106 IG-like.
FT MOD_RES 1 1 Pyrolytic carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON_TER 111
SQ SEQUENCE 111 AA; 11650 MW; 94520309932623B8 CRC64;

Query Match 41.1%; Score 236.5; DB 1; Length 111;
Best Local Similarity 44.1%; Pred. No. 1.6e-15;
Matches 49; Conservative 21; Mismatches 40; Indels 1; Gaps 1;

OY 1 QAVVQESALTTSPGRTVLTFCRSSTGAVTNSANWVQEKPDHFTGLIGGTINRPGV 60
DB 1 QSVLTQPSVSGTSGQRTVITSCGSSSN-GANNVWYQQLPGTAPKLIHTTNQPSGV 78
OY 61 PARFGSLIGDKALTTGAQTEDBAIYFCAIM--YSNHWVFGGKTLTVLG 110
DB 61 PERFGSKSGPSASLVISGLQSEDEAFYCAAMDSDLGPPYFGTGKTVTVLG 131

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 15.0885 Seconds
(without alignments)
701.451 Million cell updates/sec

Title: US-10-774-076-5

Perfect score: 576
Sequence: 1 QAVVTQESALTTSPGERTVTL.....ALMTSNHMFVGGGTRKLTIVLG 110

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	553	96.0	128	2	S52450	Ig lambda chain V
2	553	96.0	287	4	PC4402	pe1b leader/Ig hea
3	551	95.7	129	1	LIMS43E	Ig lambda-1 chain
4	546	94.8	214	2	PC4156	Ig lambda chain V
5	535.5	93.0	112	2	S06818	Ig lambda chain V
6	532	92.4	113	2	S06819	Ig lambda chain V
7	522	90.6	106	2	S20654	Ig lambda chain V
8	522	90.6	113	2	B54256	Ig lambda-1 chain
9	520.5	90.4	114	2	S06820	Ig lambda chain V
10	514	89.2	129	1	L2MS35	Ig lambda-2 chain
11	512	88.9	113	2	S06821	Ig lambda chain V
12	511.5	88.8	114	2	S06822	Ig lambda chain V
13	498	86.5	99	2	S14582	Ig lambda chain V
14	489.5	85.0	99	2	PH1089	Ig lambda chain V
15	487	84.5	97	2	PH1090	Ig lambda chain V
16	487	84.5	116	1	L1MSV	Ig lambda-1 chain
17	486	84.4	100	2	PH1088	Ig lambda chain V
18	481	83.5	99	2	S14584	Ig lambda chain V
19	471	81.8	100	2	PH1087	Ig lambda chain V
20	468	81.2	99	2	S14586	Ig lambda chain V
21	467	81.1	99	2	S14583	Ig lambda chain V
22	460	79.9	117	1	L2MSWE	Ig lambda-2 chain
23	457	79.3	99	2	S14585	Ig lambda chain V
24	448	77.8	92	2	A27633	Ig lambda-2 chain
25	416	72.2	116	2	C27390	Ig lambda chain pr
26	317.5	55.1	120	2	S30528	Ig lambda chain V
27	308.5	53.6	136	2	S42610	ARKV1 lambda protein
28	289.5	50.3	235	2	S25749	Ig lambda chain -
29	282	49.0	112	2	S26655	Ig lambda chain V

30	280.5	48.7	110	2	S57465	Ig lambda chain V-
31	279	48.4	117	1	LVHJ2	Ig lambda chain pr
32	279	48.4	117	2	S04526	Ig lambda chain pr
33	277	48.1	98	2	S36062	Ig lambda chain -
34	250	43.4	98	2	S36063	Ig lambda chain -
35	247.5	43.0	108	2	S38498	Ig lambda chain -
36	246.5	42.8	110	2	S57442	Ig lambda chain V-
37	244.5	42.4	111	1	LEHUST	Ig lambda chain V-
38	244.5	42.4	216	2	A42193	Ig lambda chain (B
39	243.5	42.3	109	2	S19663	Ig lambda chain V
40	241	41.8	149	2	S23626	Ig lambda chain V
41	240	41.7	213	2	S21066	Ig lambda chain V
42	240	41.7	217	2	JE0246	Ig lambda chain NI
43	239.5	41.6	233	2	S25744	Ig lambda chain -
44	238.5	41.4	203	2	S25752	Ig lambda chain -
45	237.5	41.2	188	2	S47184	Ig lambda chain -

ALIGNMENTS

RESULT 1

S52450

Ig lambda chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S52450

R:Berdoz, J.; Kraehenbuhl, J.P.

submitted to the EMBL Data Library, November 1994

A:Description: Specific amplification by the polymerase chain reaction of rearranged ge

A:Reference number: S52445

A:Accession: S52450

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-128 <BER>

A:Cross-references: EMBL:X82687, NID:9673448, PIDN:CAAS8008.1, PID:9673449

A:Inserts: 16/1

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-111/Domain: immunoglobulin homology <IMM>

Query Match 96.0%; Score 553; DB 2; Length 128;

Best Local Similarity 97.2%; Pred. No. 1.5e-41;

Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QAVVTQESALTTSPGERTVTLTCSRSTGAVTTSNAGNVQEKPDHFTGLIGTINRVGV 60

Db 20 QAVVTQESALTTSPGERTVTLTCSRSTGAVTTSNAGNVQEKPDHFTGLIGTINRVGV 79

Qy 61 PARFSGSLIGDKALTTGAQTEDEAIYFCALMTSNHMFVGGGTRKLTIVL 109

Db 80 PARFSGSLIGDKALTTGAQTEDEAIYFCALMTSNHMFVGGGTRKLTIVL 128

RESULT 2

PC4402

pe1b leader/Ig heavy chain anti-NP/1 linker type 205/alkaline phosphatase fusion protein

C:Species: synthetic

C>Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998

C:Accession: PC4402

R:Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.

J. Biochem. 122, 322-329, 1997

A>Title: Construction, bacterial expression, and characterization of haptten-specific si

A:Reference number: PC4402

A:Accession: PC4402

A:Molecule type: DNA

A:Residues: 1-287 <SUZ>

C:Keywords: fusion protein

Query Match 96.0%; Score 553; DB 4; Length 287;

Best Local Similarity 97.2%; Pred. No. 3.4e-41;

Matches 106; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGETVTLTCRSTGAVTTSNSANWQEKPDHFTGLIGTINRPGV 60
 DB 26 QAVTQESALTTSPGETVTLTCRSTGAVTTSNSANWQEKPDHFTGLIGTINRPGV 85
 QY 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVGGGTCTLVG 109
 DB 86 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVGGGTCTLVG 134

RESULT 3
 LIMS4E
 Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43)
 C/Species: Mus musculus (house mouse)
 C/Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
 C/Accession: B93815, B93775, A93784, C93784, A90780, C93282, A01995
 R/Burstein, Y.; Schechter, I.
 Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
 A/Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursor
 A/Reference number: A93815, MUID:77148916, PMID:403522
 A/Contents: MOPC 104E
 A/Accession: B93815
 A/Molecule type: protein
 A/Residues: 1-29 <BDR>
 A/Cross-references: UNIPROT:P01724
 A/Note: this precursor was synthesized in a cell-free system directed by messenger RNA
 R/Adpella, E.
 Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
 A/Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
 A/Reference number: A93775, MUID:71107854, PMID:5276767
 A/Contents: MOPC 104E; RPC 20
 A/Accession: B93775
 A/Molecule type: protein
 A/Residues: 'Z', 21-25, 'Q', 27-129 <APR>
 A/Accession: C93775
 A/Molecule type: protein
 A/Residues: 20-129 <APZ>
 A/Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E
 R/Cesarri, I.M.; Weigert, M.
 Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
 A/Title: Mouse lambda-chain sequences
 A/Reference number: A93784, MUID:73229669, PMID:4516208
 A/Contents: J558, S104, S178
 A/Accession: A93784
 A/Molecule type: protein
 A/Residues: 20-129 <CRS>
 A/Accession: B93784
 A/Molecule type: protein
 A/Residues: 20-129 <CR2>
 A/Accession: C93784
 A/Molecule type: protein
 A/Residues: 20-43, 'N', 45-70, 'N', 72-115, 'R', 117-129 <CR3>
 A/Note: these proteins were isolated from serum or urine of tumor-bearing mice
 R/Bernard, O.; Horumi, N.; Tongawa, S.
 Cell 15, 1133-1144, 1978
 A/Title: Sequences of mouse immunoglobulin light chain genes before and after somatic ch
 A/Reference number: A90780, MUID:79084170, PMID:103630
 A/Contents: H2020
 A/Accession: A90780
 A/Molecule type: DNA
 A/Residues: 1-43, 'T', 45-50, 'G', 52-58, 'E', 60-89, 'D', 91-129 <BER>
 A/Note: the sequence was determined from the differentiated gene
 R/Bochwell, A.L.M.; Parkind, M.; Rehn, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
 Nature 298, 380-382, 1982
 A/Title: Somatic variants of murine immunoglobulin lambda light chains.
 A/Reference number: A93282, MUID:8220143, PMID:6283385
 A/Contents: S43
 A/Accession: C93282
 A/Molecule type: DNA
 A/Residues: 1-58, 'E', 60-89, 'D', 91-98, 'T', 100-105, 'M', 107-129 <BOT>
 A/Note: the sequence was determined from the differentiated gene
 C/Comment: The MOPC 104E sequence is shown.

C/Genetics:
 A/Incons: 16/1
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k-
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; pyroglytamic acid
 F/1-19/Domain: signal sequence #status experimental <SIG>
 F/20-129/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>
 F/34-111/Domain: immunoglobulin homology <IMM>
 F/20/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experime
 F/41-109/Disulfide bonds: #status predicted

Query Match 95.7%; Score 551; DB 1; Length 129;
 Best Local Similarity 95.5%; Pred. No. 2, 3e-41;
 Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGETVTLTCRSTGAVTTSNSANWQEKPDHFTGLIGTINRPGV 60
 DB 20 QAVTQESALTTSPGETVTLTCRSTGAVTTSNSANWQEKPDHFTGLIGTINRPGV 79

QY 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVGGGTCTLVG 110
 DB 80 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVGGGTCTLVG 129

RESULT 4
 PC4156
 Ig lambda chain V region MabB23 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
 C/Accession: PC4156
 R/Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
 Gene 169, 237-239, 1996
 A/Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
 A/Reference number: PC4155, MUID:96194809, PMID:8647454
 A/Accession: PC4156
 A/Molecule type: mRNA
 A/Residues: 1-214 <KMA>
 A/Cross-references: GB:U28967, NID:91262178, PIDN:AAC52488.1; PID:91262179
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 F/1-214/Product: light chain #status predicted <MAT>
 F/98-110/Region: V region
 F/130-198/Domain: immunoglobulin homology <IMM>

Query Match 94.8%; Score 546; DB 2; Length 214;
 Best Local Similarity 95.5%; Pred. No. 1e-40;
 Matches 105; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGETVTLTCRSTGAVTTSNSANWQEKPDHFTGLIGTINRPGV 60
 DB 1 QAVTQESALTTSPGETVTLTCRSTGAVTTSNSANWQEKPDHFTGLIGTINRPGV 60

QY 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVGGGTCTLVG 110
 DB 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVGGGTCTLVG 110

RESULT 5
 S06818
 Ig lambda chain V region - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 C/Accession: S06818
 R/Miller III, A.; Glaseel, J.A.
 J. Mol. Biol. 209, 763-778, 1989
 A/Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mo
 A/Reference number: S06815, MUID:90064531, PMID:2555519
 A/Accession: S06818
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-112 <ML>
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

F.15-92/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 535.5; DB 2; Length 112;
Best Local Similarity 94.5%; Pred. No. 4, 4e-40;
Matches 104; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 2 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 60
DB 1 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 60
QY 61 PARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTLTVLG 110
DB 61 PARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTLTVLG 110

RESULT 6

Ig lambda chain V region (clone 10C3) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C/Accession: S06819
R/Miller III, A.; Glaeser, J.A.
J. Mol. Biol. 209, 763-778, 1989
A/Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor
A/Reference number: S06815; MUID:90064531; PMID:2555519
A/Accession: S06819

A/Molecule type: mRNA

A/Residues: 1-113 <MIL>

A/Cross-references: EMBL:X17168; NID:G52251; PIDN:CAA35046.1; PID:G930172

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F.15-92/Domain: immunoglobulin homology <IMM>

F.121-89/Disulfide bonds: #status predicted

Query Match 92.4%; Score 532; DB 2; Length 113;
Best Local Similarity 95.4%; Pred. No. 9, 1e-40;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 61
DB 1 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 60
QY 62 ARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTLTVL 109
DB 61 ARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTLTVL 108

RESULT 7

S20654

Ig lambda chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C/Accession: S20654

R/Lozman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A/Description: Relationships among antinuclear antibodies from autoimmune MRL mice react

A/Reference number: S20635

A/Accession: S20635

A/Status: Preliminary

A/Molecule type: DNA

A/Residues: 1-106 <LOS>

A/Cross-references: EMBL:X65012; NID:G52705; PIDN:CAA46145.1; PID:G952706

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F.15-92/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 522; DB 2; Length 106;
Best Local Similarity 94.3%; Pred. No. 6, 4e-39;
Matches 100; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 QAVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 60
DB 1 QAVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 60

QY 61 PARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTL 106
DB 61 PARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTL 106

RESULT 8

B54256

Ig lambda-1 chain V region (hybridoma Se155-4) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C/Accession: B54256; A44592

R/Bundle, D.R.; Eichler, E.; Gidney, M.A.; Meldal, M.; Ragunathas, A.; Sigurdskjold, B.W.

Biochemistry 33, 5172-5182, 1994

A/Title: Molecular recognition of a salmonella trisaccharide epitope by monoclonal anti-

A/Reference number: A54256; MUID:94227048; PMID:751555

A/Accession: B54256

A/Molecule type: Protein

A/Residues: 1-113 <BUN>

A/Experimental source: Se155-4 hybridoma, BALB/C mouse

A/Note: sequence extracted from NCBI database (NCBI:146746)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F.15-92/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 522; DB 2; Length 113;
Best Local Similarity 90.0%; Pred. No. 6, 8e-39;
Matches 99; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QAVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 60
DB 1 QAVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 60
QY 61 PARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTLTVLG 110
DB 61 PARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTLTVLG 110

RESULT 9

S06820

Ig lambda chain V region (clone 12D4) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C/Accession: S06820

R/Miller III, A.; Glaeser, J.A.

J. Mol. Biol. 209, 763-778, 1989

A/Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor

A/Reference number: S06815; MUID:90064531; PMID:2555519

A/Accession: S06820

A/Molecule type: mRNA

A/Residues: 1-114 <MIL>

A/Cross-references: EMBL:X17169

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F.15-92/Domain: immunoglobulin homology <IMM>

F.122-90/Disulfide bonds: #status predicted

Query Match 90.4%; Score 520.5; DB 2; Length 114;
Best Local Similarity 94.5%; Pred. No. 9, 2e-39;
Matches 103; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 60
DB 1 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWQEKPDHFTGLIGGTINRPGV 60
QY 61 PARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTLTVL 109
DB 61 PARFGSLIGDKAALTTTGAQTEDEAIYFCALWYSNHWVFGGKTLTVL 109

RESULT 10

L2MS35

Ig lambda-2 chain precursor V region (MOPC 315) - mouse
C/Species: Mus musculus (house mouse)

C/Date: 31-Mar-1980 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C/Accession: A93431; B93282; B91462; A90372; A90410; S09391; A01997

R/nu, G.E.; Govindji, N.; Hozumi, N.; Murialdo, H.
Nucleic Acids Res. 10, 3831-3843, 1982

A/Title: Nucleotide sequence of a chromosomal rearranged lambda-2 immunoglobulin gene of
A/Reference number: A93431; MUID:82274221; PMID:6287422

A/Accession: A93431
A/Molecule type: mRNA

A/Residues: 1-129 <MUG>

A/Cross-references: UNIPROT:P01729

R/Botwell, A.L.M.; Parkind, M.; Rech, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D

Nature 298, 380-382, 1982

A/Title: Somatic variants of murine immunoglobulin lambda light chains.
A/Reference number: A93282; MUID:82220143; PMID:6283385

A/Accession: B93282
A/Molecule type: DNA

A/Residues: 1-129 <BOT>

A/Note: the sequence was determined from the differentiated gene
R/Schechter, I.; Wolf, O.; Zemell, R.; Bursstein, Y.
Fed. Proc. 38, 1839-1845, 1979

A/Title: Structure and function of immunoglobulin genes and precursors.
A/Reference number: A91462; MUID:79148758; PMID:428562

A/Accession: B91462
A/Molecule type: protein

A/Residues: 1-22 <SCH>

R/Dugan, E.S.; Bradshaw, R.A.; Simms, E.S.; Eisen, H.N.
Biochemistry 12, 5400-5416, 1973

A/Title: Amino acid sequence of the light chain of a mouse myeloma protein (MOPC-315).
A/Reference number: A90372; MUID:74048693; PMID:4760498

A/Accession: A90372
A/Molecule type: protein

A/Residues: 20-24, 'E', '26-73', 'D', '75-129' <DUG>

R/Gavish, M.; Zakut, R.; Wilchek, M.; Givol, D.
Biochemistry 17, 1345-1351, 1978

A/Title: Preparation of a semisynthetic antibody.
A/Reference number: A90410; MUID:78187254; PMID:418802

A/Accession: A90410
A/Molecule type: protein

A/Residues: 1-129 <GAV>

R/Bogen, B.; Lambiris, J.D.
EMBO J. 8, 1947-1952, 1989

A/Title: Minimum length of an idiotype peptide and a model for its binding to a major H
A/Reference number: S09391; MUID:9005397; PMID:2732076

A/Accession: S09391
A/Molecule type: protein

A/Residues: 110-126 <BOG>

C/Comment: This chain is from a myeloma protein with anti-DNP activity.

C/Species: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; pyroglutamic acid

F/1-19/Domain: signal sequence #status experimental <SIG>
F/20-129/Domain: Ig lambda-2 chain precursor V region #status experimental <MAT>

F/34-111/Domain: immunoglobulin homology <IMM>

F/110-126/Region: idiotype to histocompatibility complex class II #status experimental
F/20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental

F/41-109/Disulfide bonds: #status predicted

Query Match 89.2%; Score 514; DB 1; Length 129;
Best Local Similarity 88.2%; Pred. No. 3.9e-38;

Matches 97; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 QAVTQESALTTSPGETVTLTCRSSTGAVTTSNANWQKPKHLFTGLIGTINRPGV 60

DB 20 QAVTQESALTTSPGETVTLTCRSSTGAVTTSNANWQKPKHLFTGLIGTINRPGV 79

QY 61 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALWYSNHWFGGGTKLTVLG 110

DB 80 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALWYSNHWFGGGTKLTVLG 129

RESULT 11

S06821
Ig lambda chain V region (clone 11C7) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C/Accession: S06821

R/Miller III, A.; Glaseel, J.A.
J. Mol. Biol. 209, 763-778, 1989

A/Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor
A/Reference number: S06815; MUID:90064531; PMID:2555519

A/Accession: S06821
A/Molecule type: mRNA

A/Residues: 1-113 <MTL>

A/Cross-references: EMBL:X17170; NID:G52253; PIDN:CA35048.1; PID:G930174
A/Note: The authors translated the codon AGT for residue 47 as Gln, GGT for residue 56

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

F/14-91/Domain: immunoglobulin homology <IMM>
F/21-89/Disulfide bonds: #status predicted

Query Match 88.3%; Score 512; DB 2; Length 113;
Best Local Similarity 90.8%; Pred. No. 5.1e-38;

Matches 99; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 2 AVTQESALTTSPGETVTLTCRSSTGAVTTSNANWQKPKHLFTGLIGTINRPGV 61

DB 1 AVTQESALTTSPGETVTLTCRSSTGAVTTSNANWQKPKHLFTGLIGTINRPGV 60

QY 62 ARFSGSLIGDKKALTTTGAQTEDEAIYFCALWYSNHWFGGGTKLTVLG 110

DB 61 ARFSGSLIGDKKALTTTGAQTEDEAIYFCALWYSNHWFGGGTKLTVLG 109

RESULT 12

S06822
Ig lambda chain V region (clone 3B9) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C/Accession: S06822

R/Miller III, A.; Glaseel, J.A.
J. Mol. Biol. 209, 763-778, 1989

A/Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mor
A/Reference number: S06815; MUID:90064531; PMID:2555519

A/Accession: S06822
A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-114 <MTL>

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match 88.8%; Score 511.5; DB 2; Length 114;
Best Local Similarity 91.8%; Pred. No. 5.7e-38;

Matches 101; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 2 AVTQESALTTSPGETVTLTCRSSTGAVTTSNANWQKPKHLFTGLIGTINRPGV 60

DB 1 AVTQESALTTSPGETVTLTCRSSTGAVTTSNANWQKPKHLFTGLIGTINRPGV 60

QY 61 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALWYSNHWFGGGTKLTVLG 110

DB 61 PARFSGSLIGDKKALTTTGAQTEDEAIYFCALWYSNHWFGGGTKLTVLG 110

RESULT 13

S14582
Ig lambda chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C/Accession: S14587; S14588
R/Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
Submitted to the EMBL Data Library, March 1991
A/Description: Natural polyclonal antibodies differ from Ag-induced antibodies in VH

A:Reference number: S1484
A:Accession: S14582
A:Molecule type: mRNA
A:Residues: 1-99 <CH>
A:Cross-references: EMBL:X58654, NID:g52911, PIDN:CAA41511.1, PID:g52912
A:Experimental source: Isolate PPC-1-54
A:Accession: S14587
A:Molecule type: mRNA
A:Residues: 1-99 <CH2>
A:Cross-references: EMBL:X58659, NID:g52921, PIDN:CAA41516.1, PID:g52922
A:Experimental source: Isolate PPC-1-5
A:Accession: S14588
A:Molecule type: mRNA
A:Residues: 1-99 <CH3>
A:Cross-references: EMBL:X58660, NID:g52923, PIDN:CAA41517.1, PID:g52924
A:Experimental source: Isolate PPC-15-30
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 86.5%; Score 498; DB 2; Length 99;
Best Local Similarity 96.0%; Pred. No. 7,4e-37;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 QAVTQESALTTSPGETVTLTCRSSTGAVTTSNANWVOEKPDHFTGLIGGTINRPGV 60
DB 1 QAVTQESALTTSPGETVTLTCRSSTGAVTTSNANWVOEKPDHFTGLIGGTINRPGV 60
OY 61 PARFSGSLIGDKAALTTGAQTEDEAIYFCALWYSNHW 99
DB 61 PARFSGSLIGDKAALTTGAQTEDEAIYFCALWYSNHW 99

RESULT 14

PH1089
Ig Lambda chain V region (clone 165.33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1089
R:Titman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0971, MUID:92381444, PMID:1512540
A:Accession: PH1089
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-99 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 489.5; DB 2; Length 99;
Best Local Similarity 96.0%; Pred. No. 4,1e-36;
Matches 96; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 1 QAVTQESALTTSPGETVTLTCRSSTGAVTTSNANWVOEKPDHFTGLIGGTINRPGV 60
DB 1 QAVTQESALTTSPGETVTLTCRSSTGAVTTSNANWVOEKPDHFTGLIGGTINRPGV 60
OY 61 PARFSGSLIGDKAALTTGAQTEDEAIYFCALWYSNHW 100
DB 61 PARFSGSLIGDKAALTTGAQTEDEAIYFCALWYSNHW 99

RESULT 15

PH1090
Ig Lambda chain V region (clone V-lambda-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1090
R:Titman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0971, MUID:92381444, PMID:1512540
A:Accession: PH1090
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-97 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 487; DB 2; Length 97;
Best Local Similarity 96.9%; Pred. No. 6,6e-36;
Matches 94; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 QAVTQESALTTSPGETVTLTCRSSTGAVTTSNANWVOEKPDHFTGLIGGTINRPGV 60
DB 1 QAVTQESALTTSPGETVTLTCRSSTGAVTTSNANWVOEKPDHFTGLIGGTINRPGV 60
OY 61 PARFSGSLIGDKAALTTGAQTEDEAIYFCALWYSN 97
DB 61 PARFSGSLIGDKAALTTGAQTEDEAIYFCALWYSN 97

Search completed: December 29, 2004, 18:06:57
Job time : 16.2552 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OW protein - protein search, using sw model

Run on: December 29, 2004, 18:05:34 ; Search time 63.5988 Seconds
(without alignments)
622.182 Million cell updates/sec

Title: US-10-774-076-5

Perfect score: 576
Sequence: 1 QAVVTQSALITSGEFTVTL.....ALWYSNMHVFSGGKTLTVLG 110

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 159051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 159051

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	576	100.0	110	Sequence 5, Appl1
2	559	97.0	112	Sequence 8, Appl1
3	555	96.4	110	Sequence 21, Appl1
4	540	93.8	110	Sequence 1, Appl1
5	535	92.9	109	Sequence 21, Appl1
6	535	92.9	109	Sequence 29, Appl1
7	532	92.4	109	Sequence 22, Appl1
8	532	92.4	109	Sequence 27, Appl1
9	531	92.2	109	Sequence 23, Appl1
10	531	92.2	109	Sequence 28, Appl1
11	530.5	92.1	109	Sequence 7, Appl1
12	530.5	92.1	109	Sequence 7, Appl1
13	530	92.0	108	Sequence 4, Appl1

14	522	90.6	391	14	US-10-328-190-14	Sequence 14, Appl1
15	519	90.1	129	16	US-10-768-193-8	Sequence 8, Appl1
16	519	90.1	218	16	US-10-379-192-159	Sequence 159, App
17	517	89.8	109	10	US-09-940-727B-1	Sequence 1, Appl1
18	513	89.1	109	10	US-09-940-727B-2	Sequence 2, Appl1
19	508	88.2	107	14	US-10-328-190-10	Sequence 10, Appl1
20	504	87.5	109	10	US-09-940-727B-3	Sequence 3, Appl1
21	504	87.5	109	10	US-09-940-727B-121	Sequence 121, App
22	494	85.8	218	16	US-10-379-392-164	Sequence 164, App
23	493	85.6	218	16	US-10-379-392-161	Sequence 161, App
24	473	82.1	99	10	US-09-940-727B-92	Sequence 92, Appl1
25	469	81.4	99	10	US-09-940-727B-88	Sequence 88, Appl1
26	428	74.3	100	10	US-09-940-727B-96	Sequence 96, Appl1
27	421	73.1	112	16	US-10-327-898-809	Sequence 809, App
28	413.5	71.8	98	10	US-09-940-727B-4	Sequence 4, Appl1
29	391.5	68.0	252	9	US-09-750-424-1	Sequence 1, Appl1
30	391.5	68.0	252	14	US-10-169-179-1	Sequence 1, Appl1
31	338	58.7	245	10	US-09-880-748-1523	Sequence 1523, App
32	338	58.7	245	14	US-10-293-418-1523	Sequence 1523, App
33	329	57.1	108	10	US-09-848-798-51	Sequence 51, Appl1
34	329	57.1	108	10	US-09-848-798-52	Sequence 52, Appl1
35	329	57.1	108	10	US-09-848-798-166	Sequence 166, App
36	315.5	54.8	253	14	US-10-322-673-54	Sequence 54, Appl1
37	315	54.7	108	10	US-09-848-798-53	Sequence 53, Appl1
38	309	53.6	216	9	US-09-291-299A-8	Sequence 8, Appl1
39	303.5	52.7	249	10	US-09-880-748-1838	Sequence 1838, App
40	303.5	52.7	249	14	US-10-293-418-1838	Sequence 1838, App
41	300	52.1	84	9	US-09-135-238B-5	Sequence 5, Appl1
42	294.5	51.1	244	14	US-10-120-414-77	Sequence 77, Appl1
43	292.5	50.8	251	10	US-09-880-748-890	Sequence 890, App
44	292.5	50.8	251	10	US-09-880-748-891	Sequence 891, App
45	292.5	50.8	251	10	US-09-880-748-894	Sequence 894, App

ALIGNMENTS

RESULT 1
US-10-774-076-5
Sequence 5, Application US/10774076
Publication No. US20040210040A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
TITLE OF INVENTION: Amphiregulin Anticodules and Their Use to Treat Cancer and
FILE REFERENCE: 05882.0064.NPUS01
CURRENT APPLICATION NUMBER: US/10/774,076
CURRENT FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 110
TYPE: PRT
ORGANISM: mus sp.
US-10-774-076-5

Query Match 100.0%; Score 576; DB 17; Length 110;
Best Local Similarity 100.0%; Pred. No. 4e-46;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QAVVTQSALITSGEFTVTLTCSRSTGAVTTSNANWVKRPHLFTGLIGGTINRPGV 60
DB 1 QAVVTQSALITSGEFTVTLTCSRSTGAVTTSNANWVKRPHLFTGLIGGTINRPGV 60
QY 61 PARSSGLIDKALTTTGACTEDEAIFYFCALWYSNMHVFSGGKTLTVLG 110
DB 61 PARSSGLIDKALTTTGACTEDEAIFYFCALWYSNMHVFSGGKTLTVLG 110
RESULT 2
US-10-816-938-8
Sequence 8, Application US/10816938

Publication No. US20040229301A1
GENERAL INFORMATION:
APPLICANT: Wang, Baiyang
TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
FILE REFERENCE: 1861.1670002
CURRENT APPLICATION NUMBER: US/10/816,938
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 112
TYPE: PRT
ORGANISM: Mus sp.
US-10-816-938-8

Query Match 97.0%; Score 559; DB 17; Length 112;
Best Local Similarity 97.3%; Pred. No. 1.6e-44;
Matches 107; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QAVVQESALTTSPGETVTLTCRSSGTAVTTSNANWVOEKPDHLFTGLIGGTINRVPGV 60
DB 1 QAVVQESALTTSPGETVTLTCRSSGTAVTTSNANWVOEKPDHLFTGLIGGTINRVPGV 60
QY 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNNHWFGGGTGLTVLG 110
DB 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNNHWFGGGTGLTVLG 110

RESULT 3
US-10-816-938-21
Sequence 21, Application US/10816938
Publication No. US20040229301A1
GENERAL INFORMATION:
APPLICANT: Wang, Baiyang
TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
FILE REFERENCE: 1861.1670002
CURRENT APPLICATION NUMBER: US/10/816,938
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 110
TYPE: PRT
ORGANISM: Mus sp.
US-10-816-938-21

Query Match 96.4%; Score 555; DB 17; Length 110;
Best Local Similarity 96.4%; Pred. No. 3.6e-44;
Matches 106; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QAVVQESALTTSPGETVTLTCRSSGTAVTTSNANWVOEKPDHLFTGLIGGTINRVPGV 60
DB 1 QAVVQESALTTSPGETVTLTCRSSGTAVTTSNANWVOEKPDHLFTGLIGGTINRVPGV 60
QY 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNNHWFGGGTGLTVLG 110
DB 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNNHWFGGGTGLTVLG 110

RESULT 4
US-10-625-047-1
Sequence 1, Application US/10625047
Publication No. US20040198962A1
GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Cornelli, Todd
TITLE OF INVENTION: Multi-Functional Antibodies
FILE REFERENCE: 023070-130910US
CURRENT APPLICATION NUMBER: US/10/625,047
CURRENT FILING DATE: 2003-07-22
PRIORITY APPLICATION NUMBER: US 10/350,555
PRIORITY FILING DATE: 2003-01-23

NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 110
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: murine monoclonal antibody 2D12.5 light chain
US-10-625-047-1

Query Match 93.8%; Score 540; DB 17; Length 110;
Best Local Similarity 93.6%; Pred. No. 9e-43;
Matches 103; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QAVVQESALTTSPGETVTLTCRSSGTAVTTSNANWVOEKPDHLFTGLIGGTINRVPGV 60
DB 1 QAVVQESALTTSPGETVTLTCRSSGTAVTTSNANWVOEKPDHLFTGLIGGTINRVPGV 60
QY 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNNHWFGGGTGLTVLG 110
DB 61 PARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNNHWFGGGTGLTVLG 110

RESULT 5
US-10-625-047-21
Sequence 21, Application US/10625047
Publication No. US20040198962A1
GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Cornelli, Todd
TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: 023070-130910US
CURRENT APPLICATION NUMBER: US/10/625,047
CURRENT FILING DATE: 2003-07-22
PRIORITY APPLICATION NUMBER: US 10/350,555
PRIORITY FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 109
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: native hybridoma murine 2D12.5 light chain
US-10-625-047-21

Query Match 92.9%; Score 535; DB 17; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.6e-42;
Matches 102; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 AVVQESALTTSPGETVTLTCRSSGTAVTTSNANWVOEKPDHLFTGLIGGTINRVPGV 61
DB 1 AVVQESALTTSPGETVTLTCRSSGTAVTTSNANWVOEKPDHLFTGLIGGTINRVPGV 61
QY 62 ARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNNHWFGGGTGLTVLG 110
DB 62 ARFSGSLIGDKAALTTTGAQTEDEAIYFCALMYSNNHWFGGGTGLTVLG 110

RESULT 6
US-10-625-047-29
Sequence 29, Application US/10625047
Publication No. US20040198962A1
GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Cornelli, Todd
TITLE OF INVENTION: Multi-Functional Antibodies
FILE REFERENCE: 023070-130910US
CURRENT APPLICATION NUMBER: US/10/625,047

;; CURRENT FILING DATE: 2003-07-22
;; PRIOR APPLICATION NUMBER: US 10/350,555
;; PRIOR FILING DATE: 2003-01-23
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 29
;; LENGTH: 109
;; TYPE: PRT
;; ORGANISM: Mus musculus
;; FEATURE:
;; OTHER INFORMATION: native hybridoma murine 2D12.5 light chain
;; OTHER INFORMATION: variable region (VL)
US-10-625-047-29

Query Match 92.9%; Score 535; DB 17; Length 109;
Best Local Similarity 93.6%; Pred. No. 2.6e-42;
Matches 102; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWVQEKPDHFTGLIGGTINRVPGPV 61
DB 1 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNANWVQEKPDHFTGLIGGNNRPPGPV 60
QY 62 ARFSGSLIGDKAALTTGAQTDEDAIYFCALWYSNHWVFGGKTLTVLG 110
DB 61 ARFSGSLIGDKAALTTAGTQTEDEDAIYFCALWYSNHWVFGGKTLTVLG 109

RESULT 7
US-10-625-047-22
;; Sequence 22, Application US/10625047
;; Publication No. US20040198962A1
;; GENERAL INFORMATION:
;; APPLICANT: Meares, Claude
;; APPLICANT: Cornelli, Todd
;; APPLICANT: The Regents of the University of California
;; TITLE OF INVENTION: Multi-Functional Antibodies
;; FILE REFERENCE: 023070-130910US
;; CURRENT APPLICATION NUMBER: US/10/625,047
;; CURRENT FILING DATE: 2003-07-22
;; PRIOR APPLICATION NUMBER: US 10/350,555
;; PRIOR FILING DATE: 2003-01-23
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 22
;; LENGTH: 109
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:native cloned
;; OTHER INFORMATION: hybridoma murine 2D12.5 light chain variable
;; OTHER INFORMATION: region (VL)
US-10-625-047-22

Query Match 92.4%; Score 532; DB 17; Length 109;
Best Local Similarity 94.4%; Pred. No. 5e-42;
Matches 102; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWVQEKPDHFTGLIGGTINRVPGPV 61
DB 1 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNANWVQEKPDHFTGLIGGNNRPPGPV 60
QY 62 ARFSGSLIGDKAALTTGAQTDEDAIYFCALWYSNHWVFGGKTLTVL 109
DB 61 ARFSGSLIGDKAALTTAGTQTEDEDAIYFCALWYSNHWVFGGKTLTVL 108

RESULT 8
US-10-625-047-27
;; Sequence 27, Application US/10625047
;; Publication No. US20040198962A1
;; GENERAL INFORMATION:
;; APPLICANT: Meares, Claude
;; APPLICANT: Cornelli, Todd

;; APPLICANT: The Regents of the University of California
;; TITLE OF INVENTION: Multi-Functional Antibodies
;; FILE REFERENCE: 023070-130910US
;; CURRENT APPLICATION NUMBER: US/10/625,047
;; CURRENT FILING DATE: 2003-07-22
;; PRIOR APPLICATION NUMBER: US 10/350,555
;; PRIOR FILING DATE: 2003-01-23
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 27
;; LENGTH: 218
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:native cloned
;; OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
;; OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
;; OTHER INFORMATION: kappa light chain constant region (TTC1)
US-10-625-047-27

Query Match 92.4%; Score 532; DB 17; Length 218;
Best Local Similarity 94.4%; Pred. No. 1e-41;
Matches 102; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWVQEKPDHFTGLIGGTINRVPGPV 61
DB 3 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNANWVQEKPDHFTGLIGGNNRPPGPV 62
QY 62 ARFSGSLIGDKAALTTGAQTDEDAIYFCALWYSNHWVFGGKTLTVL 109
DB 63 ARFSGSLIGDKAALTTAGTQTEDEDAIYFCALWYSNHWVFGGKTLTVL 110

RESULT 9
US-10-625-047-23
;; Sequence 23, Application US/10625047
;; Publication No. US20040198962A1
;; GENERAL INFORMATION:
;; APPLICANT: Meares, Claude
;; APPLICANT: Cornelli, Todd
;; APPLICANT: The Regents of the University of California
;; TITLE OF INVENTION: Multi-Functional Antibodies
;; FILE REFERENCE: 023070-130910US
;; CURRENT APPLICATION NUMBER: US/10/625,047
;; CURRENT FILING DATE: 2003-07-22
;; PRIOR APPLICATION NUMBER: US 10/350,555
;; PRIOR FILING DATE: 2003-01-23
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 23
;; LENGTH: 109
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:N51C cloned
;; OTHER INFORMATION: mutant murine 2D12.5 light chain variable region
;; OTHER INFORMATION: (VL)
US-10-625-047-23

Query Match 92.2%; Score 531; DB 17; Length 109;
Best Local Similarity 94.4%; Pred. No. 6.2e-42;
Matches 102; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNSANWVQEKPDHFTGLIGGTINRVPGPV 61
DB 1 AVVTQESALTTSPGETVTLTCRSSSTGAVTTSNANWVQEKPDHFTGLIGGNNRPPGPV 60
QY 62 ARFSGSLIGDKAALTTGAQTDEDAIYFCALWYSNHWVFGGKTLTVL 109
DB 61 ARFSGSLIGDKAALTTAGTQTEDEDAIYFCALWYSNHWVFGGKTLTVL 108

RESULT 10

US-10-625-047-28
; Sequence 28, Application US/10625047
; Publication No. US20040198962A1
; GENERAL INFORMATION:
; APPLICANT: Meares, Claude
; APPLICANT: Cornelli, Todd
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Multi-Functional Antibodies
; FILE REFERENCE: 023070-130910US
; CURRENT APPLICATION NUMBER: US/10/625,047
; PRIORITY FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 10/350,555
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: N53C cloned
; OTHER INFORMATION: mutant chimeric murine 2012.5 light chain variable
; OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
; OTHER INFORMATION: antibody kappa light chain constant region (TTCCL)
US-10-625-047-28

Query Match 92.2%; Score 531; DB 17; Length 218;
Best Local Similarity 94.4%; Pred. No. 1.3e-41;
Matches 102; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 AVVTQESALTTSPGRTVTLTCRSSGTGAVTTSNANWVQEKPDHFTGLIGGTINRVPGV 61
DB 3 AVVTQESALTTSPGRTVTLTCRSSGTGAVTTSNANWVQEKPDHFTGLIGGTINRVPGV 62
QY 62 RPFSSGLIGDKAALTTGAQTEDEAIYFCALMYSNHWVFGGTGLTVLG 109
DB 63 RPFSSGLIGDKAALTTGAQTEDEAIYFCALMYSNHWVFGGTGLTVLG 110

RESULT 11
US-09-865-483-7
; Sequence 7, Application US/09865483
; Patent No. US2002006181A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SI
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/09/865,483
; PRIORITY FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-865-483-7

Query Match 92.1%; Score 530.5; DB 9; Length 109;
Best Local Similarity 93.6%; Pred. No. 6.9e-42;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
QY 1 QAVVTQESALTTSPGRTVTLTCRSSGTGAVTTSNANWVQEKPDHFTGLIGGTINRVPGV 60
DB 1 QAVVTQESALTTSPGRTVTLTCRSSGTGAVTTSNANWVQEKPDHFTGLIGGTINRVPGV 60
QY 61 RPFSSGLIGDKAALTTGAQTEDEAIYFCALMYSNHWVFGGTGLTVLG 110
DB 61 RPFSSGLIGDKAALTTGAQTEDEAIYFCALMYSNHWVFGGTGLTVLG 109

RESULT 12
US-10-726-555-7

; Sequence 7, Application US/10726555
; Publication No. US20040191259A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Jong Wook et al.
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV S-SI
; FILE REFERENCE: 1599-0197P
; CURRENT APPLICATION NUMBER: US/10/726,555
; PRIORITY FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US/09/865,483
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-726-555-7

Query Match 92.1%; Score 530.5; DB 17; Length 109;
Best Local Similarity 93.6%; Pred. No. 6.9e-42;
Matches 103; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 QAVVTQESALTTSPGRTVTLTCRSSGTGAVTTSNANWVQEKPDHFTGLIGGTINRVPGV 60
DB 1 QAVVTQESALTTSPGRTVTLTCRSSGTGAVTTSNANWVQEKPDHFTGLIGGTINRVPGV 60
QY 61 RPFSSGLIGDKAALTTGAQTEDEAIYFCALMYSNHWVFGGTGLTVLG 110
DB 61 RPFSSGLIGDKAALTTGAQTEDEAIYFCALMYSNHWVFGGTGLTVLG 109

RESULT 13
US-10-305-268-4
; Sequence 4, Application US/10305268
; Publication No. US20030124057A1
; GENERAL INFORMATION:
; APPLICANT: GRIFPETHS, GARY L.
; APPLICANT: HANSEN, HANS J.
; APPLICANT: GOVINDAN, SERENGULAM V.
; APPLICANT: LOSMAN, MICHELLE
; APPLICANT: OU, ZHENGXING
; TITLE OF INVENTION: ANTI-DOTA ANTIBODY
; FILE REFERENCE: 18733/1154
; CURRENT APPLICATION NUMBER: US/10/305,268
; PRIORITY FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/333,479
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: LGIVL amino acid sequence
US-10-305-268-4

Query Match 92.0%; Score 530; DB 14; Length 108;
Best Local Similarity 92.6%; Pred. No. 7.6e-42;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 VVTQESALTTSPGRTVTLTCRSSGTGAVTTSNANWVQEKPDHFTGLIGGTINRVPGV 62
DB 1 VVTQESALTTSPGRTVTLTCRSSGTGAVTTSNANWVQEKPDHFTGLIGGTINRVPGV 60
QY 63 RPFSSGLIGDKAALTTGAQTEDEAIYFCALMYSNHWVFGGTGLTVLG 110
DB 61 RPFSSGLIGDKAALTTGAQTEDEAIYFCALMYSNHWVFGGTGLTVLG 108

RESULT 14

US-10-328-190-14
 ; Sequence 14, Application US/10328190
 ; Publication No. US20030162709A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSSI, EDMOND A.
 ; APPLICANT: CHANG, CHIEH-HSING KEN
 ; APPLICANT: GOLDBERG, DAVID M.
 ; TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
 ; TITLE OF INVENTION: FROM VH AND VL DOMAINS
 ; FILE REFERENCE: 042418/0115
 ; CURRENT APPLICATION NUMBER: US/10/328,190
 ; CURRENT FILING DATE: 2003-04-03
 ; PRIOR APPLICATION NUMBER: 60/342,103
 ; PRIOR FILING DATE: 2001-12-26
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 391
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Protein
 ; OTHER INFORMATION: Sequence for VL-chain of TSI
 US-10-328-190-14

Query Match 90.6%; Score 522; DB 14; Length 391;
 Best Local Similarity 90.0%; Pred. No. 1.7e-40;
 Matches 99; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGETVTLTCRSSTGAVTTSNSANWVOEKPDHLFTGLIGGTINRVPGV 60
 DB 152 QTVVTOESALTTSPGETVTLTCRSSTGAVTTSNSANWVOEKPDHLFTGLIGGTINRVPGV 211
 QY 61 PARFSGSLIGDKALTTTGAQTDEDAIYFCALWYSNHVWFGGKTLVTLG 110
 DB 212 PARFSGSLIGDKALTTTGAQTDEDAIYFCALWYSNHVWFGGKTLVTLG 261

RESULT 15
 US-10-768-193-8
 ; Sequence 8, Application US/10768193
 ; Publication No. US20040181042A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
 ; APPLICANT: YANAGISAWA, Katsuhiko
 ; APPLICANT: SHIBATA, Masao
 ; TITLE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
 ; TITLE OF INVENTION: amyloid b-protein and DNA encoding the antibody
 ; FILE REFERENCE: P0102402
 ; CURRENT APPLICATION NUMBER: US/10/768,193
 ; CURRENT FILING DATE: 2004-02-02
 ; PRIOR APPLICATION NUMBER: JP P2001-235700
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: PCT/JP02/07874
 ; PRIOR FILING DATE: 2002-08-01
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 129
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-768-193-8

Query Match 90.1%; Score 519; DB 16; Length 129;
 Best Local Similarity 90.0%; Pred. No. 9.7e-41;
 Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QAVVTOESALTTSPGETVTLTCRSSTGAVTTSNSANWVOEKPDHLFTGLIGGTINRVPGV 60
 DB 20 QAVVTOESALTTSPGETVTLTCRSSTGAVTTSNSANWVOEKPDHLFTGLIGGTINRVPGV 79
 QY 61 PARFSGSLIGDKALTTTGAQTDEDAIYFCALWYSNHVWFGGKTLVTLG 110

DB 80 PARFSGSLIGDKALTTTGAQTDEDAIYFCALWYSNHVWFGGKTLVTLG 129

Search completed: December 29, 2004, 18:42:00
 Job time : 64.5988 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:38:43 ; Search time 80.0708 Seconds
(Without alignments)
833.556 Million cell updates/sec

Title: US-10-774-076-4

Perfect score: 617
Sequence: 1 EVGLQSGALVRSASVRL.....YGGTTFAYWGGTIVTVA 116

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UnIProt 02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	489.5	79.3	466	2 099131	Q99131 mus musculu
2	439.5	71.2	109	2 099185	Q99185 mus musculu
3	413.5	67.0	473	2 099184	Q99184 mus musculu
4	408.5	66.2	614	2 077M76	Q77M76 mus musculu
5	407	66.0	139	2 0924R5	Q924R5 mus musculu
6	407	66.0	465	2 06PUB2	Q6PUB2 mus musculu
7	407	66.0	465	2 AAh18280	AAh18280 mus muscu
8	403.5	65.4	120	1 HV03 MOUSE	P01747 mus musculu
9	401	65.0	118	2 0921C4	Q921C4 mus musculu
10	401	65.0	139	1 HV07 MOUSE	P01751 mus musculu
11	401	65.0	145	2 0924G7	Q924G7 mus musculu
12	400.5	64.9	140	1 HV02 MOUSE	P01746 mus musculu
13	400	64.8	136	2 07TPE3	Q7TPE3 mus musculu
14	398	64.5	145	2 0924R1	Q924R1 mus musculu
15	397.5	64.4	146	2 0924R8	Q924R8 mus musculu
16	396	64.2	124	2 0924G6	Q924G6 mus musculu
17	394	63.9	145	2 0924Q9	Q924Q9 mus musculu
18	394	63.9	145	2 0924Q9	Q924Q9 mus musculu
19	394	63.9	473	2 099125	Q99125 mus musculu
20	392.5	63.6	140	2 0924R2	Q924R2 mus musculu
21	392.5	63.6	142	2 0924Q1	Q924Q1 mus musculu
22	392	63.5	143	2 0924P9	Q924P9 mus musculu
23	391	63.4	143	2 091V67	Q91V67 mus musculu
24	391	63.4	145	2 0924R4	Q924R4 mus musculu
25	390.5	63.3	142	2 0924Q2	Q924Q2 mus musculu
26	390	63.2	141	2 0924Q4	Q924Q4 mus musculu
27	390	63.2	145	2 0924R3	Q924R3 mus musculu
28	389.5	63.2	488	2 091W81	Q91W81 mus musculu
29	389.5	63.1	146	2 0924Q3	Q924Q3 mus musculu
30	389.5	63.1	489	2 08VCK4	Q8VCK4 mus musculu
31	389	63.0	143	2 0924R0	Q924R0 mus musculu

32	389	63.0	145	2 0924P7	Q924P7 mus musculu
33	389	63.0	482	2 08K172	Q8K172 mus musculu
34	387.5	62.8	481	2 091W71	Q91W71 mus musculu
35	387	62.7	137	2 0924R6	Q924R6 mus musculu
36	386.5	62.6	146	2 0924Q8	Q924Q8 mus musculu
37	385.5	62.5	472	2 06PJA7	Q6PJA7 mus musculu
38	385.5	62.5	472	2 AAh18535	AAh18535 mus muscu
39	384.5	62.3	144	2 0924P5	Q924P5 mus musculu
40	384.5	62.3	464	2 AAh19337	AAh19337 homo sapi
41	384	62.2	143	2 0924R7	Q924R7 mus musculu
42	384	62.2	463	2 0991C4	Q991C4 mus musculu
43	383.5	62.2	480	2 06P089	Q6P089 homo sapien
44	383.5	62.2	480	2 AAh65733	AAh65733 homo sapi
45	383	62.1	613	2 08VCK7	Q8VCK7 mus musculu

ALIGNMENTS

RESULT 1
ID 099131 PRELIMINARY; PRT; 468 AA.
AC 099131;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toohylyki S., Carninci P., Prange C.,
RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,
RA Krzyzanski M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RX TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Strauberg R.,
RA Submitted (EBB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR PDB; 1A3R; X-ray; H=-.
DR PDB; 2AP2; X-ray; B/D=20-139.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
Query Match 79.3%; Score 489.5; DB 2; Length 468;
Best Local Similarity 78.5%; Pred. No. 2,3e-41;
Matches 95; Conservative 10; Mismatches 9; Indels 7; Gaps 2;
QY 1 EVOLQGSGARLVSGASVKSCTASGPNIKDYIHWKORPEQGLEWICIDPENGDTEY 60
DB 20 EVQLQSGAEVLRGASVKSCTASGPNIKDSIMHWKORPEQGLEWIMIDPEDQETKY 79
QY 61 APNFGARVMTADTSSNTAYLQLSLTSEPTAVYYC-----YGGITTFAYMGCGTLVYSA 115
DB 80 APKFKDQKATITADTSSNTAYLQLSLTSEPTAVYYCARMLLYGG--YDYMGQGGITTVS 137
QY 116 A 116
DB 138 S 138
RESULT 2
Q9UL85 PRELIMINARY; PRT; 109 AA.
AC Q9UL85;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Anti-mycosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206021; AAF69319.1; --
DR HSRP; Q99L31; 2AP2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT TER 109
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4DE CRC64;
Query Match 71.2%; Score 439.5; DB 2; Length 109;
Best Local Similarity 76.1%; Pred. No. 5,5e-37;
Matches 83; Conservative 11; Mismatches 14; Indels 1; Gaps 1;
QY 9 AELVRSASVKTSGTASGPNIKDYIHWKORPEQGLEWICIDPENGDTEYAPNFGRA 68
DB 1 AELVKKPASVKTSGTASGPNIDTYMHWKORPEQGLEWIGRIDPATGSKTDPRFGKA 60
QY 69 TMTADTSSNTAYLQLSLTSEPTAVYYC--GGITTFAYMGCGTLVYSA 116
DB 61 TITSSTSSNTAYLQLSLTSEPTAVYYCVRRGAIVFDYMGQGGITTVS 109
RESULT 3
Q9DBL4 PRELIMINARY; PRT; 473 AA.
ID Q9DBL4;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE library, clone:181006009 product:immunoglobulin heavy chain 6 (heavy
DE chain of IgM), full insert sequence.
GN Name=Igh-1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komoto H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtractions of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11078861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komoto H., Akiyama U., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ichikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotoh K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Komoto H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shitaki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBD databases.
DR EMBL; AK007918; BAB25349.1; --
DR PIR; PH165; PH165.
DR PIR; S19966; S19966.
DR PIR; S26746; S26746.

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83131846; PubMed=6186498;
 RA Sikevitz M., Gelfer M.L., Brodeur P., Riblet R.,
 Marshak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsenate
 RT idotype response of the strain A mouse.";
 RL Eur. J. Immunol. 12:1023-1032(1982).
 CC -1- MISCELLANEOUS: From analysis of the sizes of several other
 CC differentiated genes that hybridize to this one, the authors
 CC conclude that all of these V regions have rearranged to the same J
 CC segment, JH2.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PDB: 1UFG; X-ray; H=120.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IG_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM 3D-structure; Hydridoma; Immunoglobulin V region.
 FT DOMAIN 1 111 IG_1like.
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA; 13307 MW; F04BA167B654AF CRC64;
 Query Match 65.4%; Score 403.5; DB 1; Length 120;
 Best Local Similarity 64.2%; Pred. No. 2.9e-33;
 Matches 77; Conservative 17; Mismatches 21; Indels 5; Gaps 1;
 QY 2 VOLQSGAEIVRSGAVKSLCTASGFNKKDYIHWVKRPROGLEWICIDPENGDTEYA 61
 DB 1 VOLQSGAEIVRSGAVKSLCTASGFNKKDYIHWVKRPROGLEWICIDPENGDTEYA 60
 QY 62 PNFQGRATMTADTSNTAVYQLSLTSEDTAVVYC-----YGGITFAVWGQGLTVTVA 116
 DB 61 EKFGKKTTLTVDKSSSTAVYQRLSLTSEDSAVYFCARSVYGGSYFPYWGQGLTVTVA 120
 RESULT 9
 ID 0921C4 PRELIMINARY; PRT; 118 AA.
 AC 0921C4;
 DT 01-MAY-1989 (TRENBLREL. 10, Created)
 DT 01-MAY-1989 (TRENBLREL. 10, Last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
 DE Anti-porcine VCAm mAb 3F4 heavy chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Balb/c;
 RX MEDLINE=97450619; PubMed=9307060;
 RA Mueller J.P., Giamonti M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 MacIs L.A., Evans M.J.;
 RT "Humanized porcine VCAm-specific monoclonal antibodies with chimeric
 RT IgG2/04 constant regions block human leukocyte binding to porcine
 RT endothelial cells.";
 RL Mol. Immunol. 34:441-452(1997).
 CC EMBL: U78801; AAD00293.1; -.
 DR HSSP: P01751; INOB.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IG_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 118 118
 SQ SEQUENCE 118 AA; 13036 MW; 90BEC559D31EC4FC CRC64;
 Query Match 65.0%; Score 401; DB 2; Length 118;

Best Local Similarity 65.3%; Pred. No. 5.1e-33;
 Matches 77; Conservative 15; Mismatches 24; Indels 2; Gaps 1;
 QY 1 EVOLQSGAEIVRSGAVKSLCTASGFNKKDYIHWVKRPROGLEWICIDPENGDTEYA 60
 DB 1 VOLQSGAEIVRSGAVKSLCTASGFNKKDYIHWVKRPROGLEWICIDPENGDTEYA 60
 QY 61 APNQGATMTADTSNTAVYQLSLTSEDTAVVYC-----TFAVWGQGLTVTVA 116
 DB 61 TQKRGKATLTADKSSSTAVYQRLSLTSEDSAVYFCARVYGGSYFPYWGQGLTVTVA 118
 RESULT 10
 ID HV07_MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bochwel A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 Baltimore D.;
 RT "Heavy chain variable region contribution to the Npb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma
 CC making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl
 CC (Npb antibodies).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: J00529; AAA38170.1; -.
 DR PIR: A90809; MHMS18.
 DR PDB: 1A6U; X-ray; H=20-139.
 DR PDB: 1A6V; X-ray; H=20-139.
 DR PDB: 1A6W; X-ray; H=20-139.
 DR PDB: INOB; X-ray; A/C=20-139.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IG_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KM 3D-structure; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 139
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 58
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DOMAIN 118 124
 FT DOMAIN 125 139
 FT DISULFID 41 115
 FT STRAND 22 24
 FT STRAND 28 31
 FT TURN 33 34
 FT STRAND 37 44
 FT HELIX 48 50
 FT STRAND 52 58
 Ig heavy chain V region B1-8/186-2.
 Framework-1.
 Complementarity-determining-1.
 Framework-2.
 Complementarity-determining-2.
 Framework-3.
 D segment.
 JH2 SEGMENT.
 By similarity.

```
FT TURN 60 61
FT STRAND 64 70
FT TURN 72 74
FT STRAND 77 79
FT HELIX 81 83
FT TURN 84 86
FT STRAND 87 92
FT TURN 93 96
FT STRAND 97 102
FT HELIX 107 109
FT STRAND 111 118
FT TURN 120 123
FT STRAND 129 137
FT NON TER 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match
Best Local Similarity 65.0%; Score 401; DB 1; Length 139;
Matches 76; Conservative 17; Mismatches 23; Indels 4; Gaps 1;

QY 1 EVOLQOOGAELVRSASVYLSCTASGFNKKDYIHHWKORPEGLIEWIGCIDPENGDTEY 60
DB 20 QVQLQQPGAEIVRPGASVYLSCKASGYTFTSYMMHWKORPGRLGIWIGRIDPNSGGITKY 79
QY 61 APNFOGRATMTADTSNTATYQLSLTSEDTAVYVC---YGGITTFAYMGOGTLVTYSA 116
DB 80 NEKFSKATLTVDKPSSTAVYQSLTSEDSAVVYCARVDYGSSTFDYMGOGTLITVSS 139

RESULT 11
ID Q924Q7 PRELIMINARY; PRT; 145 AA.
AC Q924Q7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VHL16.2-D-J-C mu protein (Fragment).
GN Name=VHL16.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1;
DR PIR; P28833; P28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
```

```
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG_v.1.
DR PROSITE; PS50835; IG_1like; 1.
FT NON TER 1
FT NON TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match
Best Local Similarity 65.0%; Score 401; DB 2; Length 145;
Matches 76; Conservative 17; Mismatches 23; Indels 4; Gaps 1;

QY 1 EVOLQOOGAELVRSASVYLSCTASGFNKKDYIHHWKORPEGLIEWIGCIDPENGDTEY 60
DB 1 QVQLQQPGAEIVRPGASVYLSCKASGYTFTSYMMHWKORPGRLGIWIGRIDPNSGGITKY 60
QY 61 APNFOGRATMTADTSNTATYQLSLTSEDTAVYVC---YGGITTFAYMGOGTLVTYSA 116
DB 61 NEKFSKATLTVDKPSSTAVYQSLTSEDSAVVYCARVDYGSSTFDYMGOGTLITVSS 120

RESULT 12
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 9367 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00493; AAA8128.1; -.
DR PIR; A94264; HVMG57.
DR HSSP; P01747; IJFQ.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG_v.1.
DR PROSITE; PS50835; IG_1like; 1.
KW Hybridoma; Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 140 Ig heavy chain V region 9367.
FT DOMAIN 20 139 Ig-1like.
FT NON TER 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5C88 CRC64;

Query Match
Best Local Similarity 64.9%; Score 400.5; DB 1; Length 140;
Matches 77; Conservative 16; Mismatches 23; Indels 5; Gaps 1;

QY 1 EVOLQOOGAELVRSASVYLSCTASGFNKKDYIHHWKORPEGLIEWIGCIDPENGDTEY 60
DB 20 QVQLQQPGAEIVRPGASVYLSCKASGYTFTSYGIMHWKORPGRLGIWIGRIDPNSGGITKY 79
```

QY 61 APNFGAATMTADTSNTAYQLSLTSEDTAVYYC-----YGGTTFAYWGQGLTVYVS 115
 DB 80 NEKRSKATLTVDKXSSSTAYWQLSLTSEDSAVYFCARSHRYGGSYDFDYGQGLTVYVS 139
 QY 116 A 116
 DB 140 S 140

RESULT 13

QTPPE3 PRELIMINARY; PRT; 136 AA.
 AC QTPPE3;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Pseudo gene (Fragment).
 GN Name=V23-D-J-IgG1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB069864; BAC54573.1; -
 DR InterPro; IPR007110; Ig_1-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 136
 SQ SEQUENCE 136 AA; 14882 MW; 99392B1A31F663AF CRC64;

Query Match 64.8%; Score 400; DB 2; Length 136;
 Best Local Similarity 65.8%; Pred. No. 7.6e-33;
 Matches 77; Conservative 12; Mismatches 24; Indels 4; Gaps 1;

QY 4 LQSGAEIVRSAGSVKLSCTASGFNIKDYIHWKQREQGLEWIGCTIDPENGDTVEYFN 63
 DB 1 LQSGAEIVRSAGSVKLSCTASGFNIKDYIHWKQREQGLEWIGCTIDPENGDTVEYFN 60
 QY 64 FQGRATMTADTSNTAYQLSLTSEDTAVYYC-----YGGTTFAYWGQGLTVYVS 116
 DB 61 FKSRAATLTVDKXSSSTAYWQLSLTSEDSAVYFCARSHRYGGSYDFDYGQGLTVYVS 117

RESULT 14

Q924R1 PRELIMINARY; PRT; 145 AA.
 AC Q924R1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 GN Name=VH186.2-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067789; BAB63274.1; -
 DR PIR; F28833; F28833.
 DR PIR; F33932; F33932.
 DR PIR; PH1105; PH1105.

DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR InterPro; IPR007110; Ig_1-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;

Query Match 64.5%; Score 398; DB 2; Length 145;
 Best Local Similarity 64.2%; Pred. No. 1.3e-33;
 Matches 77; Conservative 17; Mismatches 22; Indels 4; Gaps 2;

QY 1 EVQLQSGAEIVRSAGSVKLSCTASGFNIKDYIHWKQREQGLEWIGCTIDPENGDTVEY 60
 DB 1 EVQLQSGAEIVRSAGSVKLSCTASGFNIKDYIHWKQREQGLEWIGCTIDPENGDTVEY 60
 QY 61 APNFGAATMTADTSNTAYQLSLTSEDTAVYYC-----YGGTTFAYWGQGLTVYVS 116
 DB 61 NEKRSKATLTVDKXSSSTAYWQLSLTSEDSAVYFCARSHRYGGSYDFDYGQGLTVYVS 120

RESULT 15

Q924R8 PRELIMINARY; PRT; 146 AA.
 AC Q924R8;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 GN Name=VH186.2-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067789; BAB63266.1; -
 DR PIR; F28833; F28833.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.

DR	PIR	PHI137	PHI137	
DR	PIR	PHI139	PHI139	
DR	PIR	PHI142	PHI144	
DR	PIR	PHI144	PHI144	
DR	PIR	PHI147	PHI147	
DR	PIR	PHI149	PHI149	
DR	PIR	PHI150	PHI150	
DR	PIR	PHI151	PHI151	
DR	PIR	PHI152	PHI152	
DR	PIR	PHI153	PHI153	
DR	InterPro	IP0007110	IG_1like	
DR	InterPro	IP0003596	IG_v	
DR	Pfam	PF00047	IG_1	
DR	SMART	SM00483	IG_1	
DR	PROSITE	PS00835	IG_LIKE	
FT	NOX_TER	1	1	
SO	SEQUENCE	146 AA	146	16216 MW

Query Match	64.4%	Score 397.5;	DB 2,	Length 146;
Best Local Similarity	63.8%	Pred. No. 1.5e-32;		
Matches 76,	Conservative 18,	Mismatches 22,	Indels 5,	Gaps 2,

```

Qy      1  EVOLQSGAEIYVSGASVTLSCASAFNKKDIYIHVWQRPQEGLEWICGCDPENGDEY  60
      2  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1  QVQLQQPGAEIYVPGASVTLSCKASGYPTSTYMHWMVQRPERGLEWIGRIDPNSGGTKY  60
      2  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      61  AHPQPGATMTADTSSNTAYIQLSLTSEDAVYYC---YGGT-TPAVWGQGLVTVS  115
      2  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61  NEKFKSAITLVDPKSTAYIMQLSLTSEDSAYVTCASSTYSSSLPYDIDWGQGLTVS  120
      2  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      116  A 116
      2  : 121
Db      121  S 121

```

```
Search completed: December 29, 2004, 18:05:18
Job time : 80.0708 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 15.9115 Seconds
(without alignments)
701.451 Million cell updates/sec

Title: US-10-774-076-4

Perfect score: 617
Sequence: 1 EVQLQSGAEIVRSGASVKL.....YGGITFRAYWGQGLTVTVSA 116

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	516.5	83.7	118	2 S25174	ig heavy chain V r
2	500.5	81.1	136	2 S04576	ig heavy chain pre
3	500	81.0	137	2 S52445	ig heavy chain V r
4	493	79.9	178	2 S29594	ig gamma chain (MM
5	487.5	79.0	120	2 S03471	ig heavy chain V-D
6	478	77.5	116	2 S15672	ig heavy chain V r
7	474.5	76.9	117	2 S17586	ig heavy chain V r
8	474	76.8	122	2 S06823	ig heavy chain V r
9	470.5	76.3	115	2 S03482	ig heavy chain V-D
10	460.5	74.6	221	2 S49220	ig heavy chain V-D
11	456.5	74.0	120	2 S03484	ig heavy chain V-D
12	453.5	73.5	107	2 PH1013	ig heavy chain V r
13	453	73.4	268	2 A56446	ig heavy chain V r
14	451.5	72.4	233	2 JCS322	ig gamma chain V r
15	446.5	72.3	108	2 JCS322	p53 specific singl
16	446	72.3	115	2 PH1012	ig heavy chain V r
17	446	72.3	115	2 PH1012	ig heavy chain V r
18	443	71.8	123	2 PH1403	ig heavy chain V r
19	442	71.6	118	2 G37267	ig heavy chain V r
20	439	71.2	114	2 A41721	nitrophenyl phosph
21	436.5	70.7	249	2 S41374	single chain Fv an
22	428	69.4	288	2 S29690	ig heavy chain V r
23	426.5	69.1	119	2 E30562	ig heavy chain V r
24	424.5	68.8	119	2 D30562	ig heavy chain V r
25	424.5	68.8	119	2 C30562	ig heavy chain V r
26	422.5	68.5	138	2 S21810	ig heavy chain V r
27	420.5	68.2	246	2 S38950	ig gamma chain - m
28	420.5	68.2	446	2 S40295	ig gamma-2a chain
29	416	67.4	107	2 A27646	ig heavy chain V r

30	413	66.9	120	2 S41394	ig heavy chain V r
31	410	66.5	469	2 S37483	ig gamma-2a chain
32	408.5	66.2	140	2 PH1482	ig heavy chain V r
33	406.5	65.9	117	2 UC2289	PL7-6 antibody hea
34	406	65.8	137	2 E29380	ig heavy chain pre
35	403	65.3	118	2 C30560	ig heavy chain V r
36	403	65.3	139	2 PS0024	ig heavy chain pre
37	402	65.2	135	2 A30577	ig heavy chain pre
38	401	65.0	116	2 S53751	antibody Fab Jcl 1
39	401	65.0	120	2 B22769	ig heavy chain V r
40	401	65.0	139	1 MEMS18	ig heavy chain pre
41	401	65.0	287	4 PC4402	pelb leader/ig hea
42	400.5	64.9	140	1 HVM5G7	ig heavy chain pre
43	399.5	64.7	117	2 G45722	anti-glycoprotein
44	399.5	64.7	120	2 S25175	ig heavy chain V r
45	398.5	64.6	116	2 S55542	ig heavy chain V r

ALIGNMENTS

```
RESULT 1
S25174
ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S25174; S31133
R:Konestler, M.; Faay, T.M.; Isoman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A:Description: Structure and binding properties of monoclonal antibodies to core histon
A:Reference number: S25174
A:Accession: S25174
A:Status: preliminary
A:Statue: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <MON>
A:Cross-references: EMBL:X67622; NID:G51854; PIDN:CAA47880.1; PID:G938259
A:Cross-references: EMBL:X67622; NID:G51854; PIDN:CAA47880.1; PID:G938259
A:Accession: S31133
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <MON>
A:Cross-references: EMBL:X67622; NID:G51854; PIDN:CAA47880.1; PID:G938259
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMV>

Query Match      83.7%; Score 516.5; DB 2; Length 118;
Best Local Similarity 84.7%; Pred. No. 5e-41;
Matches 100; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY      1 EVQLQSGAEIVRSGASVKLSCTASGPNIKDYITHWKORPEQGLENTGCIIDPENGPTXY 60
DB      1 EIDLOQSGAEIVRSGASVKLSCTASGPNIDYIHWKORPEQGLENTGCIIDPENGPTXY 60
QY      61 APPFGQATITADTSSTAYLQSLSTSEPTAYVYCGGRT---TPAYWGQGLTVTVS 115
DB      61 ASRFQGRATITADTSSTAYLQSLSTSEPTAYVYCGGRT---TPAYWGQGLTVTVS 118

RESULT 2
S04576
ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04576
R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; T
Eur. J. Immunol. 17, 91-95, 1987
A:Title: Molecular analysis of the murine lupus-associated anti-self response: involvem
A:Reference number: S04576; MUID:87133856; PMID:3102255
A:Accession: S04576
A:Molecule type: mRNA
A:Residues: 1-136 <KOF>
A:Cross-references: EMBL:X14624; NID:G52029; PIDN:CAA32777.1; PID:G52030
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```

C/Keywords: heterotetramer; immunoglobulin
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 500.5; DB 2; Length 136;
 Best Local Similarity 83.8%; Pred. No. 1.8e-39;
 Matches 98; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 1 EVOLQSGAEIVRSAGSVKLSCTASGPNIKDYIHHWKORPEQGLEWIGCIDPENGDTEY 60
 DB 20 EVOLQSGAEIVRSAGSVKLSCTASGPNIKDYIHHWKORPEQGLEWIGCIDPENGDTEY 79
 QY 61 APNFGKATMTADTSSNTAYLQSLTSEDTAVYYCYG-GTTPAYWGQGLVTVSA 116
 DB 80 ASKFOGKATMTADTSSNTAYLQSLTSEDTAVYYCTTGAYAMDYWGQGLVTVSS 136

RESULT 3

S52445

Ig heavy chain V region precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

R/Berdoz, J.; Kraehenbuhl, J.P.

A/Description: The EMBL Data Library, November 1994

A/Reference number: S52445

A/Accession: S52445

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-137 <BER>

A/Cross-references: EMBL:X82690; NID:9673439; PIDN:CA458011.1; PID:9673440

C/Genetics:

A/Insertion: 16/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-115/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 500; DB 2; Length 137;
 Best Local Similarity 82.2%; Pred. No. 2e-39;
 Matches 97; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVOLQSGAEIVRSAGSVKLSCTASGPNIKDYIHHWKORPEQGLEWIGCIDPENGDTEY 60
 DB 20 EVOLQSGAEIVRSAGSVKLSCTASGPNIKDYIHHWKORPEQGLEWIGCIDPENGDTEY 79
 QY 61 APNFGKATMTADTSSNTAYLQSLTSEDTAVYYC--YGGITTFAYWGQGLVTVSA 116
 DB 80 DPKFOGKATMTADTSSNTAYLQSLTSEDTAVYYCAVYGTSTWPFYWGQGLVTVSA 137

RESULT 4

S29594

Ig gamma chain (MM65) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

R/Seymour, R.

A/Reference number: S29594

A/Accession: S29594

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-178 <SEY>

A/Cross-references: EMBL:X57857; NID:952590; PIDN:CA440992.1; PID:952591

C/Keywords: immunoglobulin

Query Match 79.9%; Score 493; DB 2; Length 178;
 Best Local Similarity 80.5%; Pred. No. 1.2e-38;
 Matches 95; Conservative 8; Mismatches 13; Indels 2; Gaps 1;

QY 1 EVOLQSGAEIVRSAGSVKLSCTASGPNIKDYIHHWKORPEQGLEWIGCIDPENGDTEY 60

DB 14 EVOLQSGAEIVRSAGSVKLSCTASGPNIKDYIHHWKORPEQGLEWIGCIDPENGDTEY 73
 QY 61 APNFGKATMTADTSSNTAYLQSLTSEDTAVYYCYG-GTTPAYWGQGLVTVSA 116
 DB 74 DPKFOGKATMTADTSSNTAYLQSLTSEDTAVYYCTTGAYAMDYWGQGLVTVSS 131

RESULT 5

S03471

Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

R/Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milestein, C.; Theze, J.; Fougereau, M

EMBO J. 2, 867-872, 1983

A/Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-G γ

hypervariable regions

A/Reference number: S03471; MUID:84057768; PMID:6416834

A/Accession: S03471

A/Molecule type: mRNA

A/Residues: 7-120 <ROCI>

A/Cross-references: EMBL:X01820; NID:951833; PIDN:CA425962.1; PID:91333983

A/Note: This sequence was determined from the differentiated gene

J. Immunol. 129, 2554-2558, 1982

A/Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not s

A/Reference number: S07453; MUID:83058021; PMID:6815271

A/Accession: S07453

A/Molecule type: protein

A/Residues: 1-43 <ROCI>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 487.5; DB 2; Length 120;
 Best Local Similarity 79.8%; Pred. No. 2.5e-38;
 Matches 95; Conservative 8; Mismatches 13; Indels 3; Gaps 1;

QY 1 EVOLQSGAEIVRSAGSVKLSCTASGPNIKDYIHHWKORPEQGLEWIGCIDPENGDTEY 60
 DB 1 EVOLQSGAEIVRSAGSVKLSCTASGPNIKDYIHHWKORPEQGLEWIGCIDPENGDTEY 60
 QY 61 APNFGKATMTADTSSNTAYLQSLTSEDTAVYYCYG-GTTPAYWGQGLVTVSA 116
 DB 61 DPKFOGKATMTADTSSNTAYLQSLTSEDTAVYYCAVYGTSTWPFYWGQGLVTVSS 119

RESULT 6

S15672

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

R/Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris,

Bio/Technology 9, 266-271, 1991

A/Title: Resolving a human monoclonal antibody to inhibit human respiratory syncytial vi

A/Reference number: S15672; MUID:91337412; PMID:1367535

A/Accession: S15672

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-116 <TEM>

A/Cross-references: EMBL:X58835; NID:951978; PIDN:CA441644.1; PID:951979

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 478; DB 2; Length 116;
 Best Local Similarity 78.3%; Pred. No. 1.8e-37;
 Matches 90; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 2 EVOLQSGAEIVRSAGSVKLSCTASGPNIKDYIHHWKORPEQGLEWIGCIDPENGDTEY 61

Db 2 VOLQXSGTELEBRSGASVLTCTASGAFNKKDYHMMKQRPQGGHEWIGMIDPENDVDQYA 61

QY 62 PNFQGRATMTADTSNTAYVQLSLTSEDTAVYCYCGGTFITFAWGGGTLVTSA 116

Db 62 PKFGKATMTADTSNTAYVQLSLTSEDTAVYFCNSWGSDFDHMGQGTIVTSS 116

RESULT 7

1g heavy chain V region (E8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

A:Accession: S17586

R:MyVaaganam, S.E.; Peterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.

J: Mol. Biol. 221, 455-462, 1991

A:Title: Biochemical implications from the variable gene sequences of an anti-cytochrome forms.

A:Reference number: S17586; MUID:92015240; PMID:1656053

A:Accession: S17586

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-117 <MY>

A:Cross-references: EMBL:X60683; NID:951820; PIDN:CAA43095.1; PID:951821

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IM>

Query Match 76.9%; Score 474.5; DB 2; Length 117;

Best Local Similarity 77.5%; Pred. No. 3.9e-37;

Matches 93; Conservative 10; Mismatches 10; Indels 7; Gaps 2;

QY 1 EVOLQOSGAEILVRSGASVKTCTASGFNIKDYIHHVYKQREPGLEWIGCIDPENGDTEY 60

Db 1 EVOLQOSGAEILVRSGASVKTCTASGFNIKDYHMHVYKQREPGLEWIGRIDPAGNTKY 60

QY 61 APNFGRAATMTADTSNTAYVQLSLTSEDTAVYCC---YGGTITFAWGGGTLVTSA 116

Db 61 DPKQKQDKATITADTSNTAYVQLSLTSEDTAVYCCAGVDYG---NFDYWGQGTITVTSS 117

RESULT 8

S06823

1g heavy chain V region (clone IIC) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: S06823

R:Miller III, A.; Glaesel, J.A.

J: Mol. Biol. 209, 763-778, 1989

A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morf

A:Reference number: S06815; MUID:90064531; PMID:2555519

A:Accession: S06823

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-122 <MI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-99/Domain: immunoglobulin homology <IM>

Query Match 76.8%; Score 474; DB 2; Length 122;

Best Local Similarity 77.9%; Pred. No. 4.5e-37;

Matches 95; Conservative 8; Mismatches 13; Indels 6; Gaps 2;

QY 1 EVOLQOSGAEILVRSGASVKTCTASGFNIKDYIHHVYKQREPGLEWIGCIDPENGDTE 59

Db 1 EVOLQOSGAEILVRSGASVKTCTASGFNIKDYHMHVYKQREPGLEWIGRIDPANGNTK 60

QY 60 YAPNFGRAATMTADTSNTAYVQLSLTSEDTAVYCCG---TITFAWGGGTLVTV 114

Db 61 YDPKFGKATITADTSNTAYVQLSLTSEDTAVYCCARGMVLRDAMGVDPYWGQGTIVTV 120

QY 115 SA 116

Db 121 SS 122

ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)

503482
C:Species: Mus musculus (house mouse)
C:Variate: strain BALB/c
C:Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C:Accession: S03482; S07453
R:Rocca-Serra, J.; Matthews, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A:Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GR hypervariable regions.
A:Reference number: S03471; MUID:84057768; PMID:6416834
A:Accession: S03482
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 10-115 <ROC1>
A:Cross-references: EMBL:X03219
A:Note: This sequence was determined from the differentiated gene
R:Rocca-Serra, J.; Mazie, J.C.; Moliner, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougereau, M.
J. Immunol. 129, 2554-2558, 1982
A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not affect the diversity of the mouse gamma-chains anti-GR repertoire.
A:Reference number: S07453; MUID:83058021; PMID:6815271
A:Accession: S07453
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-43 <ROC2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 470.5; DB 2; Length 115;
Best Local Similarity 79.1%; Pred. No. 8.9e-37;
Matches 91; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

Qy 1 EVQIQSGAEIVRSGASVKLSCTASGFNIDYIHMKORPEQGLEWIGCIDPENGDTEY 60
1 EVQIQSGAEIVRSGASVKLSCTASGFNIDYIHMKORPEQGLEWIGRIDPAKGVTKY 60
Db 61 DPKFGKATITTDSSNTAYLQFSLTSEDTAVYYCARGTGVGRDYGQGTTLTV 115
61 APNFGKATMTADTSSNTAYLQSLTSEDTAVYYC-YGGTTFAYNGQGLTVTV 114

RESULT 10
S49220
ig gamma-1 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C:Accession: S49220
R:Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A:Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A:Reference number: S49220
A:Accession: S49220
A:Molecule type: mRNA
A:Residues: 1-221 <KIP>
A:Cross-references: EMBL:Z37502; NID:9541778; PIDN:CAA85732.1; PID:9541779
A:Experimental source: strain Balb/c
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-120/Domain: V region #status predicted <VRG>
F:121-221/Domain: C region #status predicted <CRG>
F:139-203/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 460.5; DB 2; Length 221;
Best Local Similarity 75.0%; Pred. No. 1.5e-35;
Matches 90; Conservative 12; Mismatches 13; Indels 5; Gaps 2;

Qy 1 EVQIQSGAEIVRSGASVKLSCTASGFNIDYIHMKORPEQGLEWIGCIDPENGDTEY 60
1 EVQIQSGAEIVRSGASVKLSCTASGFNIDYIHMKORPEQGLEWIGRIDPAKGVTKY 60
Db 1 QVKLBSGAEIVRSGASVKLSCTASGFNIDYIHMKORPEQGLEWIGRIDPAKGVTKY 60

```

Oy      76.3%; Score 470.5; DB 2; Length 115;
Query Match Similarity 75.0%; Pred. No. 8.9e-37;
Best Local Similarity 11%; Pred. No. 8.9e-37;
Matches 91; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

Db      1 EVOLQSGAEIVKSGASVKLSCTASGNINIKDYTHMKORPEQGLEMTGCTIDPENGDTREY 60
       |||||
1 EVOLQSGAEIVKSGASVKLSCTASGNINIKDYTHMKORPEQGLEMTIGRIDPAKGNTKY 60

Oy      61 APNFGSRTATPADSSNTAYVQLSSLTSEPTAVYYC-YGGITTFAYWQGGLTLTV 114
       |||||
61 DPKFGSKATTITDTSSTAYLQFSSLTSEDIAVYYCARGITTVGRVDYGQGITLV 115

RESULT 10
S49220
Iq gamma-1 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C:Accession: S49220
R:KiPP, B.; Becker, W.P.; Schlaak, M.M.,
submitted to the EMBL Data Library, September 1994
A:Description: Cloning and expression of a recombinant mouse Fab-fragment recog
A:Reference number: S49220
A:Accession: S49220
A:Molecule type: mRNA
A:Residues: 1-221 <Kit>
A:Cross-references: EMBL:Z37502; NID:9541778; PIDN:CAAB5732.1; PID:9541779
A:Experimental source: Strain Balb/C
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F.11-120/Domain: V region #status predicted <VRG>
F.112-221/Domain: C region #status predicted <CRG>
F.113-203/Domain: Immunoglobulin homology <IMM>

Query Match          74.6%; Score 460.5; DB 2; Length 221;
Best Local Similarity 75.0%; Pred. No. 1.5e-35;
Matches 90; Conservative 12; Mismatches 13; Indels 5; Gaps 2;

Oy      1 EVQLQQGAELIVRGASVKLSCTASGNINDYTHMKORPEQGLEMTIGCTIDPENGDREY 60
       :::::
1 QVKLDSGAELIVKSGASVKLSCTASGNINKDTYTHMKORPEQGLEMTIGRIDPANGETIKY 60

Db      1 EVQLQQGAELIVRGASVKLSCTASGNINDYTHMKORPEQGLEMTIGRIDPANGETIKY 60

```

QY 61 APNFGRAATMTADTSSNTAYLQLSLTSEDTAVYYC---YGGTTFPAVWGQGLTVTVA 116
Db 61 DPFQGGATITADTSSNTAYLQLSLTSEDTAVYYCVRGCGSS-QEPYWGQGLTVTVA 119

RESULT 11

S03484
Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C/Species: Mus musculus (house mouse)
A/Variety: strain BALB/c
C/Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C/Accession: S03484; S07453
R/Rocca-Serra, J.; Matches, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A/Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT hypervariable regions.
A/Reference number: S03471; MUID:84057768; PMID:6416834
A/Accession: S03484
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 10-120 <ROC1>
A/Cross-references: EMBL:X07144
A/Note: this sequence was determined from the differentiated gene
R/Rocca-Serra, J.; Mazie, J.C.; Moutier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougereau, J. Immunol. 129, 2554-2558, 1982
A/Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not seem to be related to the diversity of the mouse gamma-chains anti-GAT repertoire
A/Reference number: S07453; MUID:83058021; PMID:6815271
A/Accession: S07453
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-43 <ROC2>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 456.5; DB 2; Length 120;
Best Local Similarity 75.6%; Pred. No. 1.9e-35;
Matches 90; Conservative 8; Mismatches 18; Indels 3; Gaps 1;

QY 1 EVOLQSGAEIVRSGAVKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDPTEY 60
Db 1 EVOLQSGAEIVRSGAVKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPANKNSKY 60
QY 61 APNFGRAATMTADTSSNTAYLQLSLTSEDTAVYYC---YGGTTFPAVWGQGLTVTVA 116
Db 61 DPFQGGATITADTSSNTAYLQLSLTSEDTAVYYCVRGCGSS-QEPYWGQGLTVTVA 119

RESULT 12

PH1013
Ig heavy chain V region (clone 111.67) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: PH1013
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell differentiation
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH1013
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-107 <TIL>
A/Experimental source: B cell, strain [NZB x NZW]P1
C/Keywords: immunoglobulin V region; immunoglobulin homology
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.5%; Score 453.5; DB 2; Length 107;
Best Local Similarity 83.2%; Pred. No. 3.1e-35;
Matches 89; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 1 EVOLQSGAEIVRSGAVKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDPTEY 60
Db 1 EVOLQSGAEIVRSGAVKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPANKNSKY 60

QY 61 APNFGRAATMTADTSSNTAYLQLSLTSEDTAVYYC---YGGTTFPAVWGQGLTVTVA 106
Db 61 DPFQGGATITADTSSNTAYLQLSLTSEDTAVYYCVRGCGSS-QEPYWGQGLTVTVA 107

RESULT 13

A56446
Ig heavy chain V region (3H-3H acFv) - mouse (strain BALB/c)
C/Species: Mus musculus (house mouse)
C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C/Accession: A56446
R/Teng, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the native protein
A/Reference number: A56446; MUID:95229583; PMID:7713873
A/Accession: A56446
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-268 <TAN>
A/Cross-references: GB:U20617
C/Keywords: heterotetramer; immunoglobulin

Query Match 73.4%; Score 453; DB 2; Length 268;
Best Local Similarity 76.3%; Pred. No. 9.2e-35;
Matches 90; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVOLQSGAEIVRSGAVKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDPTEY 60
Db 3 QVTLQSGAEIVRSGAVKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPANKNSKY 62
QY 61 APNFGRAATMTADTSSNTAYLQLSLTSEDTAVYYC---YGGTTFPAVWGQGLTVTVA 116
Db 63 DPFQGGATITADTSSNTAYLQLSLTSEDTAVYYCVRGCGSS-QEPYWGQGLTVTVA 120

RESULT 14

S24289
Ig gamma chain V region (US34/32) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C/Accession: S24289
R/Monchamont, B.
submitted to the EMBL Data Library, September 1991
A/Description: Cloning and sequencing of the cDNA coding for the variable regions of the gamma chain
A/Reference number: S24289
A/Accession: S24289
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-116 <MON>
A/Cross-references: EMBL:X62705; MUID:951690; PIRN:CAA44584.1; PID:G1333963
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/14-97/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 451.5; DB 2; Length 116;
Best Local Similarity 75.2%; Pred. No. 5.2e-35;
Matches 88; Conservative 13; Mismatches 13; Indels 3; Gaps 2;

QY 2 VQLOQSGAEIVRSGAVKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDPTEY 61
Db 1 VQLOQSGAEIVRSGAVKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPANKNSKY 60
QY 62 APNFGRAATMTADTSSNTAYLQLSLTSEDTAVYYC---YGGTTFPAVWGQGLTVTVA 116
Db 61 DPFQGGATITADTSSNTAYLQLSLTSEDTAVYYCVRGCGSS-QEPYWGQGLTVTVA 116

RESULT 15

JC5332
p53 specific single-chain antibody Pab421 - human
C/Species: Homo sapiens (man)
C/Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

Query Match	72.4%	Score	446.5	DB 2	Length	233	
Best Local Similarity	77.7%	Pred. NO.	3.2e-34				
Matches	87	Conservative	15	Indels	3	Gaps	1

Oy 5 QQSAAELVRSASAKLSCTASGFNIKKYIILHMKOREQCELEMGICIDPENGGTETAPNR 64
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1 QESAEALVRSASAKLSCTTSGFNINNYMHWKREQLGEMIKGRINDPENGADMTTRS 60

Oy 65 QGRATMDADSNNAYIQLSLTSSEDPNAVYCCGGITTFPAWCGCLNLVTSA 116
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 61 GVKATMDADSNNAYIQLSLTSSEDPNAVYCNAAG--MDYWQGGLTVTVSS 109

Search completed: December 29, 2004, 18:06:56
Job time : 16.0782 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:37:57 ; Search time 79,7286 Seconds
(without alignments)
521.928 Million cell updates/sec

Title: US-10-774-076-4

Perfect score: 617
Sequence: 1 EVQLQSGAEELVRSGASVYL.....YGGITTFAYWGQGLTVTSA 116

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq_23Sep04:*

1: GeneSeqp1980s:*\n2: GeneSeqp1990s:*\n3: GeneSeqp2000s:*\n4: GeneSeqp2001s:*\n5: GeneSeqp2002s:*\n6: GeneSeqp2003as:*\n7: GeneSeqp2003bs:*\n8: GeneSeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	537	87.0	122	7	ABR61864
2	537	87.0	122	8	ADQ31245
3	528	85.6	122	8	ADQ31285
4	526	85.3	243	2	AAW60769
5	523	84.8	118	2	AAW01586
6	519	84.1	116	3	AAV70787
7	516	83.6	535	2	AAW28491
8	516	83.6	535	2	AAW28492
9	514.5	83.4	119	6	ABR99635
10	511	82.8	112	2	AAW89173
11	508	82.3	124	2	AAW60566
12	506	82.0	266	8	ADH77307
13	505	81.8	120	2	AAW41387
14	505	81.8	255	2	AAW41394
15	505	81.8	281	2	AAW82744
16	505	81.8	642	2	AAW82741
17	505	81.8	666	2	AAW82745
18	503	81.5	124	2	AAW60565
19	503	81.5	124	5	ABR83941
20	503	81.5	124	6	ABG75594
21	503	81.5	124	8	ADN08039
22	502	81.4	120	8	ADK18142
23	502	81.4	120	8	ADJ54095
24	502	81.4	244	8	ADK18141
25	502	81.4	244	8	ADJ54093

ALIGNMENTS

26	502	81.4	270	2	AAW75719
27	502	81.4	556	4	AAU80040
28	502	81.4	556	4	AAU97935
29	501	81.2	136	4	AAU76694
30	501	81.2	136	4	AAW35290
31	501	81.2	553	2	AAW11508
32	501	81.2	553	2	AAW73223
33	501	81.2	553	2	AAW61960
34	501	81.2	553	4	AAW85455
35	500	81.0	137	2	AAW95948
36	498.5	80.8	254	2	AAW30117
37	498.5	80.8	254	2	AAW30119
38	498.5	80.8	254	2	AAW30123
39	498.5	80.8	254	2	AAW30121
40	496	80.4	124	2	AAW39528
41	496	80.4	124	5	AAW76632
42	496	80.4	124	6	ABO07328
43	496	80.4	124	6	ABU09037
44	496	80.4	124	8	ADH29099
45	495.5	80.3	117	4	AAW82709

RESULT 1

ABR61864
ID ABR61864 standard; protein; 122 AA.

AC ABR61864;

DT 12-SEP-2003 (first entry)

DE Mouse MAb 1A1 heavy chain variable region sequence.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

ABR61864 standard; protein; 122 AA.
ABR61864; (first entry)
Mouse MAb 1A1 heavy chain variable region sequence.
MCP-3; antiinflammatory; nephrotropic; dermatological; hepatotropic; neuroprotective; antithrombotic; antihemorrhagic; antitumor; antidiabetic; ophthalmological; vasotropic; immunomodulator; cerebroprotective; antitumor; antiparkinsonian; MAb; monoclonal antibody; 1A1.
Mus musculus.
W02003048083-A2.
12-JUN-2003.
27-NOV-2002; 2002MO-US038229.
30-NOV-2001; 2001US-0343391P.
24-MAY-2002; 2002US-0363277P.
01-AUG-2002; 2002US-0400469P.
(BIOJ) BIOGEN INC.
De Fougereolles AR, Kotelianski VE, Garber E, Reid C, WPI; 2003-532819/50.
N-PSDB; ACC84729.
Novel antibody or its antigen binding fragment that specifically binds to monocytic chemotactic protein-2 and other beta-chemokine, useful for detecting presence of beta-chemokine in sample, and blocking chemotaxis.
Example 8; Page 66; 100pp; English.
The invention relates to an antibody or its antigen binding fragment (Ab) that specifically binds to a plurality of beta-chemokines, particularly monocytic chemotactic protein-2, MCP-2 and MCP-3. The antibodies are useful in an immunoassay method for detecting the presence of a beta-chemokine in a sample, and for blocking chemotaxis. The antibodies or their Afs are useful for treating a subject suffering from a disorder

CC chosen from glomerulonephritis, scleroderma, multiple sclerosis, lupus
CC nephritis, cirrhosis, atherosclerosis, inflammatory bowel disease or
CC rheumatoid arthritis. The antibodies are also useful for treating
CC oncogenic disease or cancer, Crohn's disease, diabetic nephropathy,
CC cadheria, stroke, ulcerative colitis, coronary restenosis, Huntington's
CC disease and Parkinson's disease. The present sequence represents a murine
CC monoclonal antibody (MAb) 1A1 heavy chain variable region
XX
SQ Sequence 122 AA;

Query Match 87.0%; Score 537; DB 7; Length 122;
Best Local Similarity 84.8%; Pred. No. 3.8e-41;
Matches 106; Conservative 3; Mismatches 4; Indels 12; Gaps 2;

QY 1 EVQLQSGAEIVSGASVYLSCPSGENTKDYIHHVKRPRQGLEWIGCIDPENGDTEY 60
DB 1 EVQLQSGAEIVSGASVYLSCPSGENTKDYIHHVKRPRQGLEWIGCIDPENGDTEY 60
DB 61 APFQCKATMTADTSNTAYLQLSSITSEDTAVYICNTWAVYGYSTYGG---FAVWGQGT 117
QY 112 VTVSA 116
DB 118 VTVSS 122

RESULT 2
ADQ31245
ID ADQ31245 standard; protein; 122 AA.
XX
AC ADQ31245;
XX
DT 09-SEP-2004 (first entry)

XX Murine 1A1 heavy chain variable domain antibody protein Segid 11.

XX murine; 1A1; monocytic chemotactic protein; beta-chemokine family; MCP-3;
XX glomerulonephritis; scleroderma; cirrhosis; multiple sclerosis;
XX lupus nephritis; atherosclerosis; inflammatory bowel disease;
XX rheumatoid arthritis; inflammatory disease; fibrotic disorder; cancer;
XX immunopathological disorder; antiarteriosclerotic; antirheumatic;
XX antiinflammatory; antithumatic; cyostatic; dermatological;
XX hepatotropic; immunomodulator; nephrotropic; neuroprotective; mouse; MCP.

OS Mus musculus.
XX
XX WO2004050836-A2.
XX
XX 17-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037834.
XX
XX 27-NOV-2002; 2002US-0430007P.
XX
XX (BIOG-) BIOGEN IDEC MA INC.
XX
XX De Fougereolles AR, Kotellanski VE, Garber E, Reid C, Saldanha JW,
XX Van Viljmen H;
XX
XX WPI; 2004-461110/43.
XX
XX N-PSDB; ADQ31243.

XX New antibodies against monocytic chemotactic proteins (MCP), useful for
XX treating or preventing disorders associated with detrimental MCP
XX activity; e.g. glomerulonephritis, scleroderma, multiple sclerosis, or
XX atherosclerosis.

XX Example 9; SEQ ID NO 11; 200pp; English.

XX This invention relates to an antibody for treating or preventing
XX disorders associated with detrimental monocytic chemotactic protein (MCP)
XX activity. Specifically, it refers to humanised antibodies that bind to

CC members of the beta-chemokine family (of which MCP-1, MCP-2 and MCP-3
CC belong) and in particular antibodies that have been modelled on, and
CC modified from, the variable complementarity determining regions (CDRs) of
CC the murine 1A1 and 1A1 immunoglobulin sequences. The present invention
CC describes using these antibodies to treat or prevent diseases and
CC disorders including glomerulonephritis, scleroderma, cirrhosis, multiple
CC sclerosis, lupus nephritis, atherosclerosis, inflammatory bowel disease,
CC rheumatoid arthritis, inflammatory diseases, fibrotic disorders, cancer
CC and immunopathological disorders. Accordingly, they can be used in the
CC development of pharmaceutical compositions that exhibit
CC antirheumatic, antithumatic, antinflammatory, antirheumatic,
CC cyostatic, dermatological, hepatotropic, immunomodulator, nephrotropic
CC and neuroprotective activities. This polypeptide sequence is the murine
CC 1A1 heavy chain antibody protein of the invention.
XX
SQ Sequence 122 AA;

Query Match 87.0%; Score 537; DB 8; Length 122;
Best Local Similarity 84.8%; Pred. No. 3.8e-41;
Matches 106; Conservative 3; Mismatches 4; Indels 12; Gaps 2;

QY 1 EVQLQSGAEIVSGASVYLSCPSGENTKDYIHHVKRPRQGLEWIGCIDPENGDTEY 60
DB 1 EVQLQSGAEIVSGASVYLSCPSGENTKDYIHHVKRPRQGLEWIGCIDPENGDTEY 60
DB 61 APFQCKATMTADTSNTAYLQLSSITSEDTAVYICNTWAVYGYSTYGG---FAVWGQGT 117
QY 112 VTVSA 116
DB 118 VTVSS 122

RESULT 3
ADQ31285
ID ADQ31285 standard; protein; 122 AA.
XX
AC ADQ31285;
XX
DT 09-SEP-2004 (first entry)

XX Humanised murine 1A1 heavy chain antibody protein Segid 51.

XX 1A1; monocytic chemotactic protein; beta-chemokine family;
XX glomerulonephritis; scleroderma; cirrhosis; multiple sclerosis;
XX lupus nephritis; atherosclerosis; inflammatory bowel disease;
XX rheumatoid arthritis; inflammatory disease; fibrotic disorder; cancer;
XX immunopathological disorder; antiarteriosclerotic; antirheumatic;
XX antiinflammatory; antithumatic; cyostatic; dermatological;
XX hepatotropic; immunomodulator; nephrotropic; neuroprotective; mouse; MCP;
XX murine; humanised antibody.

OS Mus musculus.
XX
XX Synthetic.
XX
XX WO2004050836-A2.
XX
XX 17-JUN-2004.
XX
XX 25-NOV-2003; 2003WO-US037834.
XX
XX 27-NOV-2002; 2002US-0430007P.
XX
XX (BIOG-) BIOGEN IDEC MA INC.
XX
XX De Fougereolles AR, Kotellanski VE, Garber E, Reid C, Saldanha JW,
XX Van Viljmen H;
XX
XX WPI; 2004-461110/43.

XX New antibodies against monocytic chemotactic proteins (MCP), useful for
XX treating or preventing disorders associated with detrimental MCP

PT activity, e.g. glomerulonephritis, scleroderma, multiple sclerosis, or
PT atherosclerosis.
XX
PS Disclosure; SEQ ID NO 51; 200pp; English.
XX
CC This invention relates to an antibody for treating or preventing
CC disorders associated with detrimental monocyte chemotactic protein (MCP)
CC activity. Specifically, it refers to humanised antibodies that bind to
CC members of the beta-chemokine family (of which MCP-1, MCP-2 and MCP-3
CC belong) and in particular antibodies that have been modelled on, and
CC modified from, the variable complementarity determining regions (CDRs) of
CC the murine 11K2 and 1A1 immunoglobulin sequences. The present invention
CC describes using these antibodies to treat or prevent diseases and
CC disorders including glomerulonephritis, scleroderma, cirrhosis, multiple
CC sclerosis, lupus nephritis, atherosclerosis, inflammatory bowel diseases,
CC rheumatoid arthritis, inflammatory diseases, fibrotic disorders, cancer
CC and immunopathological disorders. Accordingly, they can be used in the
CC development of pharmaceutical compositions that exhibit
CC antiatherosclerotic, antiarthritic, antiinflammatory, antineoplastic,
CC cytoprotective, dermatological, hepatotropic, immunomodulator, nephrotropic
CC and neuroprotective activities. This polypeptide sequence is the
CC humanised murine 1A1 variable and constant heavy chain antibody protein
CC of the invention.
SQ
Sequence 122 AA;
Query Match 85.6%; Score 528; DB 8; Length 122;
Best Local Similarity 85.2%; Pred. No. 2.5e-40;
Matches 104; Conservative 2; Mismatches 4; Indels 12; Gaps 2;
QY 1 EVOLQSGALVRSAGSVKLSCTASGFNIDYIHVWVKORPEQGLEWIGCIDPENGPTDY 60
DB 1 EVOLQSGALVRSAGSVKLSCTASGFNIDYIHVWVKORPEQGLEWIGCIDPENGPTDY 60
QY 61 APNFGKATMTADTSSNTAVYLQSLTSEDTAVYYC--YGGTTFAYWGGTTL 111
DB 61 APNFGKATMTADTSSNTAVYLQSLTSEDTAVYYCMTWAVYGYGYSYG--FAYWGGTTL 117
QY 112 VT 113
DB 118 VT 119
RESULT 4
AAW60769
ID AAW60769 standard; protein; 243 AA.
XX
AC AAW60769;
XX
DT 08-SEP-1998 (first entry)
XX
DE Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.
XX
KM Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;
KM regulatory domain; p53 mutant; H273; W248; G281;
KM p53-dependent trans-activating activity; restoration;
KM tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;
KM cancer; re-stenosis; ss.
XX
XX Mus sp.
XX OS
XX PN WO9818825-A1.
XX PD 07-MAY-1998.
XX PF 27-OCT-1997; 97WO-FR001921.
XX PR 29-OCT-1996; 96FR-00013176.
XX (RHON) RHONE-POULENC RORER SA.
XX Bracco L, Debussche L;
XX

DR WPI: 1998-272140/24.
DR N-PSDB; AAV36236.
XX
PT Restoring p53-dependent trans-activating activity to cell containing
PT mutant p53 - by delivering single-chain antibody specific for the mutant,
PT particularly for treatment of tumours.
XX
PS Claim 5; Page 31; 54pp; French.
XX
CC The present sequence represents a single chain antibody (ScFv) designated
CC 421. The antibody binds to an epitope present in the C-terminal region of
CC the p53 protein that includes oligomerisation and regulatory domains,
CC specifically between positions 320 and 393. ScFv 421 is directed against
CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
CC introduced into cells containing a mutant p53 protein, p53-dependent
CC trans-activating activity is restored. ScFv 421 is specific for p53-
CC mutants that have lost tumour-suppressing activity and are present in
CC tumour cells. It is particularly used to treat hyper-proliferation
CC associated with these mutants (e.g. cancer and re-stenosis) but may also
CC be used in vitro for studying mechanisms of activity of p53 or its mutant
CC and to purify or detect p53
SQ
Sequence 243 AA;
Query Match 85.3%; Score 526; DB 2; Length 243;
Best Local Similarity 86.4%; Pred. No. 8.1e-40;
Matches 102; Conservative 5; Mismatches 7; Indels 4; Gaps 2;
QY 1 EVOLQSGALVRSAGSVKLSCTASGFNIDYIHVWVKORPEQGLEWIGCIDPENGPTDY 60
DB 1 EVOLQSGALVRSAGSVKLSCTASGFNIDYIHVWVKORPEQGLEWIGCIDPENGPTDY 60
QY 61 APNFGKATMTADTSSNTAVYLQSLTSEDTAVYYC--YGGTTFAYWGGTTLVSA 116
DB 61 APNFGKATMTADTSSNTAVYLQSLTSEDTAVYYCNFYGDALD--YWGQGTTLVTS 116
RESULT 5
AAW01586
ID AAW01586 standard; protein; 118 AA.
XX
AC AAW01586;
XX
DT 22-AUG-1997 (first entry)
XX
DE Lead binding MAb 14G11 heavy chain variable region.
XX
KM Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KM pharmaceutical; health care; skin treatment; pesticide; herbicide;
KM heavy metal.
XX
XX Mus musculus.
XX OS
XX PN WO9639518-A1.
XX PD 12-DEC-1996.
XX PF 05-JUN-1996; 96WO-US009258.
XX PR 05-JUN-1995; 95US-00462798.
XX PR 10-OCT-1995; 95US-00541373.
XX (BION-) BIONEERASKA INC.
XX PA
XX PI WYJie DE, Lopez O, Murray PJ;
XX WPI: 1997-043140/04.
XX DR N-PSDB; AAT58260.
XX
PT DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as lead
PT cations.
XX

CC domain deleted and replaced by a leucine zipper domain. The mutants
CC preferably also have at least part of the p53 transactivating domain
CC (amino acids 1-74) deleted and replaced by the transactivating domain
CC (74) from herpes simplex virus viral protein VP16 (amino acids 411-490)
CC or by a protein domain able to bind selectively to a transactivator,
CC especially a single-chain antibody variable domain (ScFv). The present
CC sequence is that of a specifically claimed p53 variant designated S-325
CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53
CC and a leucine zipper domain at the C-terminal. The p53 variants are more
CC active and more stable tumour suppressors and apoptosis-inducing agents
CC than wild-type p53 and are active where the wild-type protein is not,
CC i.e. they are not inactivated by dominant negative or oncogenic mutants,
CC nor by other cellular proteins (because the leucine zipper domain
CC prevents formation of inactive mixed oligomers)

CC Sequence 535 AA;

Query Match 83.6%; Score 516; DB 2; Length 535;
Best Local Similarity 84.7%; Pred. No. 1.6e-38;
Matches 100; Conservative 6; Mismatches 8; Indels 4; Gaps 2;

OY 1 EVOLQSGALVRSAGSVKLSCTASGFNIKDYTHWVKORPEQGLEWIGCTDPENGDTREY 60
DB 3 QVQLQESGAEIVGSGASVYKLSCTASGFNIKDYTHWVKORPEQGLEWIGTDPENGDTREY 62
OY 61 APNFGRAITMTADTSSNTAYVQLSLTSEDPAYVYC--YGGTITFAWVGQGLTVVSA 116
DB 63 APKFGKATMTADTSSNTAYVQLSLTSEDPAYVYC--YGGTITFAWVGQGLTVVSS 118

RESULT 8

AAW28492
ID AAW28492 standard; protein; 535 AA.

XX AAW28492;

DT 25-NOV-1997 (first entry)

DE Human p53 protein variant S-325H.

XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
KW substitution; replacement; transactivation; viral protein VP16; HSV;
KM anti-oncogene; hyperproliferation; cancer; reversion; ScFv;
tumour suppression; apoptosis; single chain antibody variable domain.

XX Homo sapiens.
OS Herpes simplex virus.
OS Synthetic.
OS Chimeric.

XX Key Location/Qualifiers
FT Misc-difference 361
FT /note= "Arg residue at position 182 of wild-type p53 has
FT been mutated to His"

XX W09704092-A1.

XX 06-FEB-1997.

XX 17-JUL-1996; 96WO-FR001111.

XX 19-JUL-1995; 95FR-00008729.

XX (RHON) RHONE POULENC RORER SA.

XX Conseiller E, Bracco L;

XX WPI; 1997-132633/12.

PT New p53 variants e.g. with oligomerisation domain replaced by leucine
PT zipper - useful for treating hyper-proliferative disorders, esp. cancer
PT and restenosis.

PS Claim 36; Page; 133pp; French.

XX Claimed variants of protein p53 have at least part of the oligomerisation
CC domain deleted and replaced by a leucine zipper domain. The mutants
CC preferably also have at least part of the p53 transactivating domain
CC (amino acids 1-74) deleted and replaced by the transactivating domain
CC (74) from herpes simplex virus viral protein VP16 (amino acids 411-490)
CC or by a protein domain able to bind selectively to a transactivator,
CC especially a single-chain antibody variable domain (ScFv). The present
CC sequence is that of a specifically claimed p53 variant designated S-325H
CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53
CC (but with Arg182 replaced by His) and a leucine zipper domain at the C-
CC terminal. The p53 variants are more active and more stable tumour
CC suppressors and apoptosis-inducing agents than wild-type p53 and are
CC active where the wild-type protein is not, i.e. they are not inactivated
CC by dominant negative or oncogenic mutants, nor by other cellular proteins
CC (because the leucine zipper domain prevents formation of inactive mixed
CC oligomers). (Note: this sequence does not appear in the specification and
CC has been produced by modifying the given sequence of variant V-325)

XX Sequence 535 AA;

Query Match 83.6%; Score 516; DB 2; Length 535;
Best Local Similarity 84.7%; Pred. No. 1.6e-38;
Matches 100; Conservative 6; Mismatches 8; Indels 4; Gaps 2;

OY 1 EVOLQSGALVRSAGSVKLSCTASGFNIKDYTHWVKORPEQGLEWIGCTDPENGDTREY 60
DB 3 QVQLQESGAEIVGSGASVYKLSCTASGFNIKDYTHWVKORPEQGLEWIGTDPENGDTREY 62
OY 61 APNFGRAITMTADTSSNTAYVQLSLTSEDPAYVYC--YGGTITFAWVGQGLTVVSA 116
DB 63 APKFGKATMTADTSSNTAYVQLSLTSEDPAYVYC--YGGTITFAWVGQGLTVVSS 118

RESULT 9

ABB99635
ID ABB99635 standard; protein; 119 AA.

XX ABB99635;

DT 28-MAR-2003 (first entry)

DE 2A2 monoclonal antibody heavy chain variable region.

XX Heavy chain; variable region; monoclonal antibody; 2A2; cathepsin B;
KW cancer; arthritis.

XX Mus sp.

XX W0200294881-A2.

XX 28-NOV-2002.

XX 02-APR-2002; 2002WO-S1000013.

XX 18-MAY-2001; 2001SI-00000132.

XX (KRKA) KRKA TOVARNA ZDRAVIL DD.

XX Koe J, Premzl A, Kopitar Jerala N, Fan X, Turk V, Bestagno M,
XX Burrone OR;

XX WPI; 2003-120791/11.

XX N-PSDB; ABV77141.

PT New neutralizing antibodies directed against Cathepsin B, useful for
PT treating and/or diagnosing a disease associated with an increased
PT cathepsin B activity or concentration, e.g. cancer or arthritis.

PS Claim 3; Fig 6; 44pp; English.

CC The present sequence represents the heavy chain variable region of the

CC murine monoclonal antibody 2A2. 2A2 is a neutralizing antibody which is
CC directed against cathepsin B. The antibody is useful for treating and
CC diagnosing a disease associated with an increased cathepsin B activity,
CC such as cancer or arthritis. The antibody is also useful for
CC manufacturing a medicament for treating or diagnosing these diseases
XX
SQ Sequence 119 AA;

Query Match 83.4%; Score 514.5; DB 6; Length 119;
Best Local Similarity 83.2%; Pred. No. 4.1e-39;
Matches 99; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY 1 EVOLQSGAEIVRSQASVKLSCTASGFNIDYIHVKORPEQGLPWIGCIDPENGDTYAP 60
DB 1 QVQLQSGAEIVRSQASVKLSCTASGFNIDYIHVKORPEQGLPWIGCIDPENGDTYAP 60
QY 61 APNFGRAITMTADSSNTATLQSLTSEPTAVYYCG--GRTTAYWGQGLTVTVS 116
DB 61 APKFRGKATMTADSSNTATLQSLTSEPTAVYYCNARRHGYENDYWGQGLTVTVS 119

RESULT 10

AAW89173
ID AAW89173 standard; peptide; 112 AA.

XX AAW89173;

DT 25-MAR-1999 (first entry)

DE Anti-p53 monoclonal antibody 421 variable heavy chain sequence.

KM Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
KM immune response; tumour associated antigen; metastatic cancer.

OS Mus sp.
OS Synthetic.

PN W09856416-A1.

PD 17-DEC-1998.

PF 09-JUN-1998; 98WO-IL000266.

PR 09-JUN-1997; 97IL-00121041.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Cohen IR, Rotter V, Wolkowicz R, Ruiz PJ, Erez-Alon N, Herkel J;
PI WPI; 1999-070296/06.

PT Use of a monoclonal antibody to a tumour-associated antigen - to induce
PT anti-tumour immunity or elicit an increased immune response to the
PT antigen.

XX Example 3; Fig 3; 47pp; English.

CC The present invention describes the use of an immunogen (A) to induce
CC anti-tumour immunity; to elicit an increased immune response to tumour
CC associated antigen (TAA) and/or to induce an immune response to mutant or
CC wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
CC (MAB) to TAA, or its fragment; (ii) a peptide based on a CDR
CC (complementarity determining region) on the heavy or light chain of MAB
CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
CC variable (V) region of MAB, in a gene delivery vehicle. The present
CC sequence represents the variable heavy chain sequence from anti-p53 MAB
CC 421. Also described is a method for generating sequence from anti-p53 MAB
CC DNA antibodies (Ab) by immunising a mammal with a MAB directed to a
CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
CC used to treat a wide variety of primary and metastatic cancers,
CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
CC to determine critical sequences in animal or plant breeding); to identify
CC bacteria and other parasites; to determine parentage; in forensic science

CC ; to isolate specific genes for DNA vaccination; in gene sequencing and
CC cloning; also possibly for activation of selected therapeutic genes in
CC plants animals and humans. (A) induce an effective anti-tumour response
CC without causing harm to the patient. The method uses (A) to generate anti
CC -TAA by exploiting the anti-idiotypic network
XX
SQ Sequence 112 AA;

Query Match 82.8%; Score 511; DB 2; Length 112;
Best Local Similarity 86.8%; Pred. No. 8e-39;
Matches 99; Conservative 4; Mismatches 7; Indels 4; Gaps 2;

QY 4 LQSGAEIVRSQASVKLSCTASGFNIDYIHVKORPEQGLPWIGCIDPENGDTYAP 63
DB 1 LQSGAEIVRSQASVKLSCTASGFNIDYIHVKORPEQGLPWIGCIDPENGDTYAP 63
QY 64 FQGRATMTADSSNTATLQSLTSEPTAVYYCG--YGRTTAYWGQGLTVTVS 115
DB 61 FQGRATMTADSSNTATLQSLTSEPTAVYYCNFYGDALD--YWGQGLTVTVS 112

RESULT 11

AA60566
ID AA60566 standard; protein; 124 AA.

XX AA60566;

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 25-APR-1995 (first entry)

DE Anti-carcinoembryonic antigen chimeric heavy chain Ab.

KM Anti-carcinoembryonic antigen chimeric antibodies; CEAs;
KM chimeric human-murine; breast or colorectal carcinoma; heavy chain.

OS Mus musculus.
OS Homo sapiens.
OS Chimeric.

PN W09419466-A2.

PD 01-SEP-1994.

PF 16-FEB-1994; 94WO-US001709.

PR 16-FEB-1993; 93US-00017570.

PA (DOMC) DOM CHEM CO.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Gourlie BB, Rixon MW, Mezes PS, Kaplan DA, Schlom J;
PI WPI; 1994-294331/36.
PI N-PSDB; AAQ71396.

PT Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis and
PT therapy of carcinoma, e.g. breast or colorectal carcinoma.

XX Claim 14; Page 53; 67pp; English.

CC AAQ71396 codes for AA60566 the antibody heavy chain region of murine-
CC human anti-carcinoembryonic antigen (CEA) chimeric antibody. Which can be
CC used in in vitro immunoassays for the detection of CEA, and monitoring of
CC tumour-associated antigen during therapy. It can also be used in vivo
CC diagnostically, or in therapy for the treatment of tumours associated
CC with colorectal and breast carcinomas, as well those of the
CC gastrointestinal tract, lung, ovary and pancreas. (Updated on 25-MAR-2003
CC to correct PW field.) (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 124 AA;

Query Match 82.3%; Score 508; DB 2; Length 124;

Best Local Similarity 81.5%; Pred. No. 1.7e-38;
Matches 101; Conservative 4; Mismatches 11; Indels 8; Gaps 2;

QY 1 EVOLQOOSGAEIVRSAGSVKLSCTASGFNIXDYIHWKORPEQGLEWIGCIDPENGDREY 60
DB 1 EVOLQOOSGAEIVRSAGSVKLSCTASGFNIXDYIHWKORPEQGLEWIGCIDPENGDREY 60

QY 61 APNFGARATMTADTSNTAYIQLSSLTSEDTAVYYC-----YGGTIT---AYWGQGT 112
DB 61 APNFGARATMTADTSNTAYIQLSSLTSEDTAVYYC-----YGGTIT---AYWGQGT 112

QY 113 TVSA 116
DB 121 TVSS 124

RESULT 12
ADH77307 standard; protein, 266 AA.

ADH77307;
15-APR-2004 (first entry)

Yeast killer toxin related anti-idiotypic scFv (H20).
variable region; anti-idiotypic antibody; yeast killer toxin;
microbial infection; viral infection; candidosis; aspergilliosis;
cryptococcosis; sporotrichosis; blastomycosis; histoplasmosis; thrush;
tuberculosis; mycobacteriosis; respiratory infection; scarlet fever;
pneumonia; impetigo; rheumatic fever; sepsis; septicaemia;
cutaneous leishmaniasis; visceral leishmaniasis; keratitis;
cystic fibrosis; typhoid fever; gastroenteritis; flu; influenza; HIV;
AIDS; H20.

Undenitified.

Key Location/Qualifiers
Misc-difference 126 /note= "Encoded by TTC"

WO2003095493-A2.

20-NOV-2003.

09-MAY-2003; 2003WO-IB002348.

10-MAY-2002; 2002GB-00010783.

(UNSI-) UNIV SIENA.
(POLO/) POLONESE L.
(CASS/) CASSONE A.

PoloneSE L, Cassone A;

WPI: 2004-012091/01.
N-PSDB; ADH77306.

New toxin-related polypeptides comprising a fragment of a variable region of an anti-idiotypic antibody which recognizes the idiope of an antibody specific for a yeast killer toxin, useful for treating microbial or viral infections.

Disclosure; SEQ ID NO 22; 70pp; English.

The invention comprises a polypeptide which contains a part of the variable region of an anti-idiotypic antibody which recognizes the idiope of an antibody specific for a yeast killer toxin. The polypeptide of the invention is useful for the treatment of microbial and viral infections, such as: candidosis, aspergilliosis, cryptococcosis, sporotrichosis, blastomycosis, histoplasmosis, thrush, tuberculosis, mycobacteriosis, respiratory infections, scarlet fever, pneumonia, impetigo, rheumatic fever, sepsis, septicaemia, cutaneous and visceral

CC leishmaniasis, keratitis, cystic fibrosis, typhoid fever, gastroenteritis
CC and haemolytic-uremic syndrome, flu, influenza or HIV/AIDS. The present
CC amino acid sequence represents an anti-idiotypic antibody (H20) of the
CC invention.

Sequence 266 AA;

Query Match 82.0%; Score 506; DB 8; Length 266;
Best Local Similarity 77.8%; Pred. No. 5.9e-38;
Matches 98; Conservative 7; Mismatches 11; Indels 10; Gaps 2;

QY 1 EVOLQOOSGAEIVRSAGSVKLSCTASGFNIXDYIHWKORPEQGLEWIGCIDPENGDREY 60
DB 3 EVOLQOOSGAEIVRSAGSVKLSCTASGFNIXDYIHWKORPEQGLEWIGCIDPENGDREY 62

QY 61 APNFGARATMTADTSNTAYIQLSSLTSEDTAVYYC-----YGGTIT---AYWGQGT 110
DB 63 APNFGARATMTADTSNTAYIQLSSLTSEDTAVYYC-----YGGTIT---AYWGQGT 122

QY 111 TVSA 116
DB 123 TVCSS 128

RESULT 13
AAW41387 standard; protein, 120 AA.

AAW41387;

02-JUN-1998 (first entry)

Anti-CEA antibody 806.077 heavy chain variable region.

Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
cancer diagnosis; complementarity determining region; heavy chain.

Synthetic.

WO9742329-A1.

13-NOV-1997.

29-APR-1997; 97WO-GB001165.

04-MAY-1996; 96GB-00009405.

14-FEB-1997; 97GB-00003103.

(ZENEC) ZENECAL LTD.

Copley CG, Edge MD, Emery SC;

WPI: 1997-558987/51.
N-PSDB; AAV17269.

Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis and therapy of cancer.

Claim 3; Page 196; 208pp; English.

This sequence is the heavy chain variable region of the antibody of the invention. The antibody is an anti-CEA (carcinoembryonic antigen) antibody (806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro diagnosis of cancer

Sequence 120 AA;

Query Match 81.8%; Score 505; DB 2; Length 120;
Best Local Similarity 80.8%; Pred. No. 3e-38;

Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLQOQSGAEIYRSGASVKTCTASGFNIKDYIHWKORPEOGLEWITGCTDPENGDTEY 60
 Db 1 EVOLQOQSGAEIYRSGASVKTCTASGFNIKDYIHWKORPEOGLEWITGCTDPENGDTEY 60

QY 61 APNFOGRATMTADTSSNTAYIQLSSLTSEDTAVVYC---YGGTTTFAYWGGGTLVTVSA 116
 Db 61 APKFRGKATLTADSSSNTAYIHLSSLTSEDTAVVYCHVLIYAGIYAMDYWGQGTSAVSS 120

RESULT 14

AAW41394
 ID AAW41394 standard; protein; 255 AA.

AC AAW41394;

DT 17-OCT-2003 (revised)
 DT 02-JUN-1998 (first entry)

DE Chimeric anti-CEA antibody 806.077 HuIgG2 Fd chain.

KM Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
 KM cancer diagnosis; complementarity determining region; Fd chain.

OS Homo sapiens.

OS Mus sp.

OS Chimeric.

PN W09742329-A1.

PD 13-NOV-1997.

PF 29-APR-1997; 97WO-GB001165.

PR 04-MAY-1996; 96GB-00009405.

PR 14-FEB-1997; 97GB-00003103.

PA (ZENEC) ZENECA LTD.

PI Copley CG, Edge MD, Emery SC;

DR WPI; 1997-558987/51.

DR N-PSDB; AAV17291.

PS Example 8; Page 102-103; 208pp; English.

CC This sequence is the HuIgG2 Fd chain region of the antibody of the
 CC invention. The antibody is an anti-CEA (carcinoembryonic antigen)
 CC antibody (806.077 Ab). Host cells or transgenic organisms transformed
 CC with DNA encoding the antibody, are used to make the antibody or
 CC conjugate. The conjugate is used in a medicament suitable for intravenous
 CC administration. The conjugate can be used for cancer therapy, selectively
 CC killing tumour cells. The antibody can be used for in vivo or in vitro
 CC diagnosis of cancer. (Updated on 17-OCT-2003 to standardise OS field)

CC Sequence 255 AA;

QY Query Match 81.8%; Score 505; DB 2; Length 255;
 Db Best Local Similarity 80.8%; Pred. No. 7e-38;
 Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLQOQSGAEIYRSGASVKTCTASGFNIKDYIHWKORPEOGLEWITGCTDPENGDTEY 60
 Db 20 EVOLQOQSGAEIYRSGASVKTCTASGFNIKDYIHWKORPEOGLEWITGCTDPENGDTEY 79

QY 61 APNFOGRATMTADTSSNTAYIQLSSLTSEDTAVVYC---YGGTTTFAYWGGGTLVTVSA 116
 Db 80 APKFRGKATLTADSSSNTAYIHLSSLTSEDTAVVYCHVLIYAGIYAMDYWGQGTSAVSS 139

RESULT 15

AAW82744
 ID AAW82744 standard; protein; 281 AA.

AC AAW82744;

DT 10-MAY-1999 (first entry)

DE Fusion protein pIC1266/8061acFvtag/his.

KM Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
 KM produg-converting enzyme; cell surface antigen; treatment; cancer;
 KM inflammation; rheumatoid arthritis; antibody; produg therapy system.

OS Synthetic.

PN W09851787-A2.

PD 19-NOV-1998.

PF 05-MAY-1998; 98WO-GB001294.

PR 10-MAY-1997; 97GB-00009421.

PA (ZENEC) ZENECA LTD.

PI Emery SC, Blakey DC;

DR WPI; 1999-059700/05.

DR N-PSDB; AAV72069.

PT New gene construct expressing conjugate of targeting agent and produg-
 PT converting enzyme - useful for, e.g. targeted production of cytotoxic
 PT drug in vivo, especially for treatment of cancer.

PS Example 16; Page 84-85; 100pp; English.

CC This sequence is a used in a method for obtaining a novel gene construct
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-
 CC targeting group (I) and a heterologous produg-converting enzyme (II),
 CC and (B) is directed to leave the cell for selective localisation at a
 CC cell surface antigen (As) recognised by (I). Delivery of (A) to a target
 CC site, then administration of (III) is used for targeted release of
 CC cytotoxic drug, specifically for treating cancer but also inflammation
 CC such as rheumatoid arthritis. In situ generation of the targeting
 CC antibody increases selectivity, reducing side effects at normal tissue.
 CC The method is applicable to any antibody-directed enzyme produg therapy
 CC system

CC Sequence 281 AA;

QY Query Match 81.8%; Score 505; DB 2; Length 281;
 Db Best Local Similarity 80.8%; Pred. No. 7.8e-38;
 Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLQOQSGAEIYRSGASVKTCTASGFNIKDYIHWKORPEOGLEWITGCTDPENGDTEY 60
 Db 23 EVOLQOQSGAEIYRSGASVKTCTASGFNIKDYIHWKORPEOGLEWITGCTDPENGDTEY 82

QY 61 APNFOGRATMTADTSSNTAYIQLSSLTSEDTAVVYC---YGGTTTFAYWGGGTLVTVSA 116
 Db 83 APKFRGKATLTADSSSNTAYIHLSSLTSEDTAVVYCHVLIYAGIYAMDYWGQGTSAVSS 142

Search completed: December 29, 2004, 17:57:29
 Job time : 82.7286 secs

Publication No. US20020193561A1
GENERAL INFORMATION:
APPLICANT: CONSELLIER, EMANUEL
BRACCO, LAURENT
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNIGAN, HENDERSON, PARABOW, GARRETT &
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,851
FILING DATE: 03-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/983,035
FILING DATE: 20-Feb-1998
APPLICATION NUMBER: PCT/FR96/01111
FILING DATE: 17-Jul-1996
APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-Jul-1995
ATTORNEY/AGENT INFORMATION:
NAME: Straus, William L.
REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
FAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-968-851-38
Query Match 83.6%; Score 516; DB 9; Length 535;
Best Local Similarity 84.7%; Pred. No. 1.6e-38;
Matches 100; Conservative 6; Mismatches 8; Indels 4; Gaps 2;
QY 1 EVQAOQSGAEIVRSAGSVKLSCTASGFINIKDYIHWKORPEQGLEWIGCIDPENGDTTEY 60
DB 3 QVQAOQSGAEIVRSAGSVKLSCTASGFINIKDYIHWKORPEQGLEWIGCIDPENGDTTEY 62
QY 61 APNFGAATMTADTSSNTAYVQLSSLTSEDTAVVYC--YGGITTFAYVGGITLVTS 116
DB 63 APKQGAATMTADTSSNTAYVQLSSLTSEDTAVVYCNYGADALD--YVGGITTVTVSS 118
RESULT 3
US-10-032-482-7
Sequence 7, Application US/10032482
Publication No. US20020197270A1
GENERAL INFORMATION:
APPLICANT: Cohen, Irun
APPLICANT: Kotter, Varda
APPLICANT: Wolkowicz, Roland
APPLICANT: Ruiz, Pedro
APPLICANT: Erez-Alon, Neta
APPLICANT: Herken, Johannes
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
TITLE OF INVENTION: IMMUNITY

FILE REFERENCE: COHEN42
CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US/09/445,602
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: PCT/IL98/00266
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: IL 121041
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 112
TYPE: PRT
ORGANISM: Mus musculus
US-10-032-482-7
Query Match 82.8%; Score 511; DB 13; Length 112;
Best Local Similarity 86.8%; Pred. No. 8.8e-39;
Matches 99; Conservative 4; Mismatches 7; Indels 4; Gaps 2;
QY 4 LQSGAEIVRSAGSVKLSCTASGFINIKDYIHWKORPEQGLEWIGCIDPENGDTTEYAPN 63
DB 1 LQSGAEIVRSAGSVKLSCTASGFINIKDYIHWKORPEQGLEWIGCIDPENGDTTEYAPN 60
QY 64 FQGRATMTADTSSNTAYVQLSSLTSEDTAVVYC--YGGITTFAYVGGITLVTS 115
DB 61 FQGRATMTADTSSNTAYVQLSSLTSEDTAVVYCNYGADALD--YVGGITTVTVSS 112
RESULT 4
US-09-564-329A-11
Sequence 11, Application US/09564329A
Patent No. US20010055751A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Wille, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/564,329A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 136
TYPE: PRT
ORGANISM: SCID Mice
US-09-564-329A-11
Query Match 82.2%; Score 507; DB 9; Length 136;

Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Cy 1 EVOLQSGAEIVRSGASVKLSCTASGFNIKDYTHWVQKREOGLWIGTIDPENGDTREY 60
Db 14 EVOLQSGAEIVRSGASVKLSCTASGFNIKDYTHWVQKREOGLWIGTIDPENGDTREY 73

Cy 61 APNFGRAITMTADTSNTAYLQLSLTSEDTAVVYCYGTTTFAYWGGLTVTSA 116
Db 74 VPKFGKATMTADTFSTNTAYLHLSLTSEDTAVVYCYGTTTFAYWGGLTVTSA 125

RESULT 5

US-09-855-153-11
Sequence 11, Application US/09855153
Patent No. US2002010266A1

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14

CURRENT FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: US/09/855.153

PRIOR FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 08/814,279

PRIOR FILING DATE: 1997-03-10

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR FILING DATE: 1998-01-12

PRIOR APPLICATION NUMBER: 60/074,675

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR FILING DATE: 1998-12-21

PRIOR APPLICATION NUMBER: 60/120,536

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 60/124,658

PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/038,261

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 09/203,939

PRIOR FILING DATE: 1998-12-02

PRIOR APPLICATION NUMBER: 09/251,835

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 09/308,503

PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 136

TYPE: PRT

ORGANISM: SCID Mice

US-09-855-153-11

Query Match 82.2%; Score 507; DB 9; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Cy 1 EVOLQSGAEIVRSGASVKLSCTASGFNIKDYTHWVQKREOGLWIGTIDPENGDTREY 60
Db 14 EVOLQSGAEIVRSGASVKLSCTASGFNIKDYTHWVQKREOGLWIGTIDPENGDTREY 73

Cy 61 APNFGRAITMTADTSNTAYLQLSLTSEDTAVVYCYGTTTFAYWGGLTVTSA 116
Db 74 VPKFGKATMTADTFSTNTAYLHLSLTSEDTAVVYCYGTTTFAYWGGLTVTSA 125

RESULT 6
US-09-854-811-11
Sequence 11, Application US/09854811
Patent No. US20020119157A1

GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14

CURRENT FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: US/09/854,811

PRIOR FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR FILING DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 136

TYPE: PRT

ORGANISM: SCID Mice

US-09-854-811-11

Query Match 82.2%; Score 507; DB 9; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Cy 1 EVOLQSGAEIVRSGASVKLSCTASGFNIKDYTHWVQKREOGLWIGTIDPENGDTREY 60
Db 14 EVOLQSGAEIVRSGASVKLSCTASGFNIKDYTHWVQKREOGLWIGTIDPENGDTREY 73

Cy 61 APNFGRAITMTADTSNTAYLQLSLTSEDTAVVYCYGTTTFAYWGGLTVTSA 116
Db 74 VPKFGKATMTADTFSTNTAYLHLSLTSEDTAVVYCYGTTTFAYWGGLTVTSA 125

RESULT 7

US-09-934-773-11
Sequence 11, Application US/09934773
Patent No. US20020136689A1

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US/09/934,773

PRIOR FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 08/814,279

PRIOR FILING DATE: 1997-03-10

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR FILING DATE: 1998-01-12

PRIOR APPLICATION NUMBER: 60/074,675

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR FILING DATE: 1998-12-21

PRIOR APPLICATION NUMBER: 60/120,536

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 60/124,658

PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/038,261

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 09/203,939

PRIOR FILING DATE: 1998-12-02

PRIOR APPLICATION NUMBER: 09/251,835

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 09/308,503

PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 136

TYPE: PRT
ORGANISM: SCID Mice
US-09-934-773-11

Query Match 82.2%; Score 507; DB 9; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

QY 1 EVOLQSGAEIVRSGASVKLSCTASGNIDYIHWKORPEQGLEWIGCIDPENGDTEY 60
DB 14 EVOLQSGAEIVRSGASVKLSCTASGNIDYIHWKORPEQGLEWIGCIDPENGDTEY 73
QY 61 APNFGKATMTADTSSNTAYIQLSITSEPTAVYCYGCTITPAWYGQGLTVVSA 116
DB 74 VPKFGKATMTADTIFSNATYIHLISITSEPTAVYCYGCTITPAWYGQGLTVVSA 125

RESULT 8

US-09-963-620-11
Sequence 11, Application US/09963620
Patent No. US20020141941A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Robert E.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/963,620
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 136
TYPE: PRT
ORGANISM: SCID Mice
US-09-963-620-11

Query Match 82.2%; Score 507; DB 9; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

QY 1 EVOLQSGAEIVRSGASVKLSCTASGNIDYIHWKORPEQGLEWIGCIDPENGDTEY 60
DB 14 EVOLQSGAEIVRSGASVKLSCTASGNIDYIHWKORPEQGLEWIGCIDPENGDTEY 73
QY 61 APNFGKATMTADTSSNTAYIQLSITSEPTAVYCYGCTITPAWYGQGLTVVSA 116
DB 74 VPKFGKATMTADTIFSNATYIHLISITSEPTAVYCYGCTITPAWYGQGLTVVSA 125

RESULT 9

US-09-855-632-11
Sequence 11, Application US/09855632
Publication No. US20030113818A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Robert E.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/09/855,632
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/308,503
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 136
TYPE: PRT
ORGANISM: SCID Mice
US-09-855-632-11

Query Match 82.2%; Score 507; DB 10; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

QY 1 EVOLQSGAEIVRSGASVKLSCTASGNIDYIHWKORPEQGLEWIGCIDPENGDTEY 60
DB 14 EVOLQSGAEIVRSGASVKLSCTASGNIDYIHWKORPEQGLEWIGCIDPENGDTEY 73
QY 61 APNFGKATMTADTSSNTAYIQLSITSEPTAVYCYGCTITPAWYGQGLTVVSA 116
DB 74 VPKFGKATMTADTIFSNATYIHLISITSEPTAVYCYGCTITPAWYGQGLTVVSA 125

RESULT 10

US-10-225-784-11
Sequence 11, Application US/10225784
Publication No. US20030113820A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Robert E.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/10/225,784
PRIOR FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US/09/564,329
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326


```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-224-720-11

Query Match      82.2%; Score 507; DB 14; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Cy 1 EVOLQSGAEIVNSGASVKSLCTASGFNIDVYYIMHWKORPEQGLEWIGCIPDENGPTDY 60
    |||||
Db 14 EVOLQSGAEIVNSGASVKSLCTASGFNIDVYYIMHWKORPEQGLEWIGCIPDENGPTDY 73
    |||||

Cy 61 APNFGKATMTADTSSNTAYLQLSLTSEDTAVYYCYGTTTFAYWGQGLTVTVA 116
    |||||
Db 74 VPKFGKATMTADTSSNTAYLQLSLTSEDTAVYYCYGTTTFAYWGQGLTVTVA 125
    |||||

RESULT 11
US-10-224-720-11
; Sequence 11, Application US/10224720
; Publication No. US20030147806A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/224,720
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US/09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-225-784-11.

Query Match      82.2%; Score 507; DB 14; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-224-720-11

Query Match      82.2%; Score 507; DB 14; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Cy 1 EVOLQSGAEIVNSGASVKSLCTASGFNIDVYYIMHWKORPEQGLEWIGCIPDENGPTDY 60
    |||||
Db 14 EVOLQSGAEIVNSGASVKSLCTASGFNIDVYYIMHWKORPEQGLEWIGCIPDENGPTDY 73
    |||||

Cy 61 APNFGKATMTADTSSNTAYLQLSLTSEDTAVYYCYGTTTFAYWGQGLTVTVA 116
    |||||
Db 74 VPKFGKATMTADTSSNTAYLQLSLTSEDTAVYYCYGTTTFAYWGQGLTVTVA 125
    |||||

RESULT 12
US-10-225-779-11
; Sequence 11, Application US/10225779
; Publication No. US20030153016A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/225,779
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-225-779-11

Query Match      82.2%; Score 507; DB 14; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
```

```
RESULT 13
US-10-374-381-11
; Sequence 11, Application US/10374381
; Publication No. US20030228318A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/374.381
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/09/564.329A
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-374-381-11

Query Match      82.2%; Score 507; DB 14; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

QY 1 EVOLQSGAEIVRSGASVYKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDTEY 60
   |||||
Db 14 EVOLQSGAEIVRSGASVYKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDTEY 73
   |||||

QY 61 APNFGKATMTADTSNTAYLQLSLTSEDTAVYYCYGTTTFAYWGGTLVTYSA 116
   |||||
Db 74 VPKFGKATMTADTSNTAYLQLSLTSEDTAVYYCYGTTTFAYWGGTLVTYSA 125
   |||||

RESULT 14
US-10-446-542-11
; Sequence 11, Application US/10446542
; Publication No. US20040018571A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/446.542
; PRIOR FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/855,153
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
```

```
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: SCID Mice
US-10-446-542-11

Query Match      82.2%; Score 507; DB 15; Length 136;
Best Local Similarity 84.5%; Pred. No. 2.5e-38;
Matches 98; Conservative 4; Mismatches 10; Indels 4; Gaps 1;
```

```
QY 1 EVOLQSGAEIVRSGASVYKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDTEY 60
   |||||
Db 14 EVOLQSGAEIVRSGASVYKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDTEY 73
   |||||

QY 61 APNFGKATMTADTSNTAYLQLSLTSEDTAVYYCYGTTTFAYWGGTLVTYSA 116
   |||||
Db 74 VPKFGKATMTADTSNTAYLQLSLTSEDTAVYYCYGTTTFAYWGGTLVTYSA 125
   |||||
```

```
RESULT 15
US-09-910-059-11
; Sequence 11, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; FILE REFERENCE: 1991-209
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; CURRENT APPLICATION NUMBER: US/09/910,059
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-910-059-11
```

```
Query Match      81.8%; Score 505; DB 9; Length 120;
Best Local Similarity 80.8%; Pred. No. 3.3e-38;
Matches 97; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

QY 1 EVOLQSGAEIVRSGASVYKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDTEY 60
   |||||
Db 1 EVOLQSGAEIVRSGASVYKLSCTASGFNIKDYIHWKORPEQGLEWIGCIDPENGDTEY 60
   |||||
```


THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:37:57 : Search time 73.5428 Seconds
(without alignments)
521.928 Million cell updates/sec

Title: US-10-774-076-3

Perfect score: 563

Sequence: 1 DIGTQSPSPSMVASLGRVT.....CLQYDEPPYFGGGTLEIK 107

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	98.8	107	8	ADE85729 Human Eph
2	556	98.8	107	8	ADL23067 Human Eph
3	554	98.4	237	7	ADE57549 Human Pro
4	554	98.4	237	7	ADDA47098 Human Pro
5	554	98.4	237	7	ADDA48668 Human Pro
6	551	97.9	355	2	AAW35125 R. pipien
7	551	97.9	355	2	AAW35129 R. pipien
8	551	97.9	358	2	AAW35127 R. pipien
9	551	97.9	358	2	AAW35130 R. pipien
10	551	97.9	360	2	AAW35128 R. pipien
11	551	97.9	379	2	AAW35126 R. pipien
12	548	97.3	214	2	AAW27089 Mouse mon
13	546	97.0	127	2	AAW27089 Mouse mon
14	546	97.0	246	4	AAW27089 Mouse mon
15	541	96.1	107	2	AAW27089 Mouse mon
16	541	96.1	107	2	AAW27089 Mouse mon
17	541	96.1	107	2	AAW27089 Mouse mon
18	541	96.1	107	2	AAW27089 Mouse mon
19	534	94.8	107	6	ABG74702 Murine mu
20	534	94.8	107	6	ABG74702 Murine mu
21	531	94.3	107	2	AAW23956 Murine mu
22	529	94.0	106	2	AAW23956 Murine mu
23	527	93.6	107	2	AAW23956 Murine mu
24	527	93.6	107	2	AAW23956 Murine mu
25	525	93.3	216	2	AAW15935 Anticbody

26	525	93.3	228	2	AAW14704 Vh-Lab-Vh
27	525	93.3	228	2	AAW14789 Vh-Lab-Vh
28	525	93.3	235	2	AAW14694 Vh-Lab-Vh
29	525	93.3	236	2	AAW14702 Vh-Lab-Vh
30	525	93.3	236	2	AAW14703 Vh-Lab-Vh
31	525	93.3	236	2	AAW14699 Vh-Lab-Vh
32	525	93.3	236	2	AAW14700 Vh-Lab-Vh
33	525	93.3	236	2	AAW14701 Vh-Lab-Vh
34	523	92.9	104	2	AAW29154 Human IGE
35	522	92.7	142	2	AAW29154 Human IGE
36	522	92.7	142	2	AAW29154 Human IGE
37	522	92.7	142	2	AAW29154 Human IGE
38	522	92.7	142	2	AAW29154 Human IGE
39	522	92.7	142	3	AAW29154 Human IGE
40	522	92.7	142	5	AAW29154 Human IGE
41	522	92.7	142	5	AAW29154 Human IGE
42	522	92.7	142	6	AAW29154 Human IGE
43	522	92.7	142	7	AAW29154 Human IGE
44	519.5	92.3	129	2	AAW09815 Pe1B-VL34
45	519.5	92.3	258	2	AAW09820 VL3418-11

ALIGNMENTS

RESULT 1	
ADL23067	
ID	ADL23067 standard; protein; 107 AA.
AC	
AD	ADL23067;
AE	
AF	
AG	
AH	
AI	
AJ	
AK	
AL	
AM	
AN	
AO	
AP	
AQ	
AR	
AS	
AT	
AV	
AW	
AX	
AY	
AZ	
BA	
BB	
BC	
BD	
BE	
BF	
BG	
BH	
BI	
BJ	
BK	
BL	
BM	
BN	
BO	
BP	
BQ	
BR	
BS	
BT	
BV	
BW	
BX	
BY	
BZ	
CA	
CB	
CC	
CD	
CE	
CF	
CG	
CH	
CI	
CJ	
CK	
CL	
CM	
CN	
CO	
CP	
CQ	
CR	
CS	
CT	
CU	
CV	
CW	
CX	
CY	
CZ	
DA	
DB	
DC	
DD	
DE	
DF	
DG	
DH	
DI	
DJ	
DK	
DL	
DM	
DN	
DO	
DP	
DQ	
DR	
DS	
DT	
DV	
DW	
DX	
DY	
DZ	
EA	
EB	
EC	
ED	
EE	
EF	
EG	
EH	
EI	
EJ	
EK	
EL	
EM	
EN	
EO	
EP	
EQ	
ER	
ES	
ET	
EU	
EV	
EW	
EX	
EY	
EZ	
FA	
FB	
FC	
FD	
FE	
FF	
FG	
FH	
FI	
FJ	
FK	
FL	
FM	
FN	
FO	
FP	
FQ	
FR	
FS	
FT	
FU	
FV	
FW	
FX	
FY	
FZ	
GA	
GB	
GC	
GD	
GE	
GF	
GG	
GH	
GI	
GJ	
GK	
GL	
GM	
GN	
GO	
GP	
GQ	
GR	
GS	
GT	
GU	
GV	
GW	
GX	
GY	
GZ	
HA	
HB	
HC	
HD	
HE	
HF	
HG	
HH	
HI	
HJ	
HK	
HL	
HM	
HN	
HO	
HP	
HQ	
HR	
HS	
HT	
HU	
HV	
HW	
HX	
HY	
HZ	
IA	
IB	
IC	
ID	
IE	
IF	
IG	
IH	
II	
IJ	
IK	
IL	
IM	
IN	
IO	
IP	
IQ	
IR	
IS	
IT	
IU	
IV	
IW	
IX	
IY	
IZ	
JA	
JB	
JC	
JD	
JE	
JF	
JG	
JH	
JI	
JJ	
JK	
JL	
JM	
JN	
JO	
JP	
JQ	
JR	
JS	
JT	
JU	
JV	
JW	
JX	
JY	
JZ	
KA	
KB	
KC	
KD	
KE	
KF	
KG	
KH	
KI	
KJ	
KL	
KM	
KN	
KO	
KP	
KQ	
KR	
KS	
KT	
KU	
KV	
KW	
KX	
KY	
KZ	
LA	
LB	
LC	
LD	
LE	
LF	
LG	
LH	
LI	
LJ	
LK	
LL	
LM	
LN	
LO	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	
LP	

CC antibody that binds EphA2 with a K-off of less than 3 x 10⁻³ s⁻¹. Also
CC described: (1) a pharmaceutical composition comprising a therapeutic
CC amount of (1) a pharmaceutical carrier; (2) a cell line that produces
CC (1); (3) a hybridoma deposited with the ATCC accession number PTA-4572,
CC PTA-4573 or PTA-4574; (4) an isolated nucleic acid comprising a
CC nucleotide sequence encoding a light chain variable domain or a heavy
CC chain variable domain of the EphA2 antibody; (5) a vector comprising the
CC methods of identifying the EphA2 agonistic antibody or the EphA2 antibody
CC that inhibits a cancer cell phenotype, that kills cancer cells having a
CC cancer cell phenotype or that preferentially binds an EphA2 epitope
CC monitoring the efficacy of therapy for cancer in a patient known to or
CC suspected to have cancer. (1) has cytostatic, antiasthmatic,
CC antiapoptotic, antiinflammatory, vasotropic and respiratory activities,
CC and can be used in gene therapy. The composition and methods are useful
CC in managing, diagnosing, preventing or treating hyperproliferative cell
CC diseases (i.e. metastatic cancer) or non-cancer hyperproliferative cell
CC diseases or disorders, such as asthma, psoriasis, inflammatory bowel
CC disease, smooth muscle restenosis, endothelial restenosis, Crohn's
CC disease or chronic obstructive pulmonary disease. They may also be used
CC for monitoring the efficacy of therapy for cancer in a patient known to
CC or suspected to have cancer, and in screening for anti-cancer drugs. The
CC present sequence is used in the exemplification of the present invention.
SQ Sequence 107 AA;

Query Match 98.8%; Score 556; DB 8; Length 107;
Best Local Similarity 98.1%; Pred. No. 5e-37;
Matches 105; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINISYLSWFOQPKSPKTLTYRANRLVDGVPS 60
DB 1 DIKMTQSPSSMYASISGERVTITCKASQDINISYLSWFOQPKSPKTLTYRANRLVDGVPS 60
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEPPYFGGSKLEIK 107
DB 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEPPYFGGSKLEIK 107

RESULT 2

ADL23067
ADL23067 standard; protein; 107 AA.

AC ADL23067;

DT 20-MAY-2004 (first entry)

DE Human EphA2 antibody VL chain.

KW antibody; human; EphA2; variable light chain; VL chain; cancer;
cytostatic.

OS Homo sapiens.

FN WO2004014292-A2.

PD 19-FEB-2004.

PF 12-MAY-2003; 2003MO-US015046.

PR 10-MAY-2002; 2002US-0379368P.

PR 14-OCT-2002; 2002US-0418204P.

PR 03-APR-2003; 2003US-0460358P.

PA (PURD) PURDUE RES FOUND.

PI Kinch MS, Carles-Kinch K;

DR WPI; 2004-180531/17.

DR N-PSDB; ADL23075.

PT Treating cancer, e.g. breast, lung, prostate, or skin cancer, comprises

PT administering an EphA2 antibody that is an EphA2 agonistic antibody or an
PT exposed EphA2 epitope antibody.
PS Claim 49; Fig 16A; 124pp; English.

CC The present invention relates to a method of treating cancer (fully or
CC partially refractory to a first treatment), comprising administering an
CC EphA2 antibody that is an EphA2 agonistic antibody or an exposed EphA2
CC epitope antibody. The method is useful for treating, managing or
CC preventing cancer (e.g. lung, colon, prostate, breast or skin cancer),
CC particularly metastatic cancer. The method may be used not only in
CC untreated patients but also in the treatment of patients partially or
CC refractory to current standard and experimental cancer therapies, e.g.
CC chemotherapies or hormonal therapies, to improve the efficacy of such
CC treatments. The present sequence is the human EphA2 antibody VL chain.
SQ Sequence 107 AA;

Query Match 98.8%; Score 556; DB 8; Length 107;
Best Local Similarity 98.1%; Pred. No. 5e-37;
Matches 105; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINISYLSWFOQPKSPKTLTYRANRLVDGVPS 60
DB 1 DIKMTQSPSSMYASISGERVTITCKASQDINISYLSWFOQPKSPKTLTYRANRLVDGVPS 60
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEPPYFGGSKLEIK 107
DB 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEPPYFGGSKLEIK 107

RESULT 3

ADE57549
ADE57549 standard; protein; 237 AA.

AC ADE57549;

DT 29-JAN-2004 (first entry)

DE Human Protein S65921, SEQ ID NO 3411.

KW Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

FN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002MO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-033347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'Urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; S65921.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 237 AA:

Query Match 98.4%; Score 554; DB 7; Length 237;
Best Local Similarity 99.1%; Pred. No. 1.6e-36;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDKMTQSPSSMYASLGSRVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
Db 23 DDKMTQSPSSMYASLGSRVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 82
61 RFGSGSGGDYSLTISLSEYEDMGIIYCYCLOYDEFPPTFGGTTLEIK 107
83 RFGSGSGGDYSLTISLSEYEDMGIIYCYCLOYDEFPPTFGGTTLEIK 129

RESULT 4

ADD47098
ID ADD47098 standard; protein; 237 AA.

AC ADD47098;
DT 29-JAN-2004 (first entry)
XX Human Protein S65921, SEQ ID NO 12766.
DE Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PI
XX
PI Woolf C, D'Urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; S65921.

XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
XX
PS Claim 1; Page; 1017P; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 237 AA:

Query Match 98.4%; Score 554; DB 7; Length 237;
Best Local Similarity 99.1%; Pred. No. 1.6e-36;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDKMTQSPSSMYASLGSRVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
Db 23 DDKMTQSPSSMYASLGSRVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 82
61 RFGSGSGGDYSLTISLSEYEDMGIIYCYCLOYDEFPPTFGGTTLEIK 107
83 RFGSGSGGDYSLTISLSEYEDMGIIYCYCLOYDEFPPTFGGTTLEIK 129

RESULT 5

ADD48668
ID ADD48668 standard; protein; 237 AA.

AC ADD48668;
DT 29-JAN-2004 (first entry)
XX Human Protein S65921, SEQ ID NO 14374.
DE Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
PA (PARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M,
PI WPI; 2003-268312/26.
XX
XX WPI; 2003-268312/26.
DR GENBANK; S65921.
XX
PT New composition comprising two or more isolated polypeptides, useful for
preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNII) in an animal (e.g. gene
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 237 AA:
SQ
Query Match 98.4%; Score 554; DB 7; Length 237;
Best Local Similarity 99.1%; Pred. No. 1.6e-36;
Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DDKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQKPKSPKTIYRANRLVDGVPS 60
DB 23 DDKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQKPKSPKTIYRANRLVDGVPS 82
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYQYDEPPYFGGTYKLEIK 107
DB 83 RFSGSGSGQDYSLTISLSEYEDMGIIYCYQYDEPPYFGGTYKLEIK 129
RESULT 6
AAW35125
ID AAW35125 standard; protein; 355 AA.
XX
XX AAW35125;
AC
XX 20-APR-1998 (first entry)
DT
XX R. pipiens recombinant RNase rOnc fusion protein 1.
DE
XX
XX RNase A; ribonuclease; cytotoxic; oncogene; nOnc; immunofusion;
KM tumour cell growth; frog.
XX
XX Rana pipiens.
OS Synthetic.

XX
XX WO9731116-A2.
XX
XX 28-AUG-1997.
XX
XX 19-FEB-1997; 97WO-US002588.
XX
XX 21-FEB-1996; 96US-0011800P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Rybak SM, Newton DL, Boque L, Wlodawer A;
XX WPI; 1997-435168/40.
XX
XX N-PSDB; AAT94963.
XX
XX Ribonuclease molecules based on native Onconase - used for killing cells,
PT particularly tumour cells.
XX
XX Disclosure; Page 67; 90pp; English.
XX
XX Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (Onc) which are modifications of the RNase Onconase (Rim) (Onc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
CC or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by selectively killing unwanted
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
XX ribonucleases have increased cytotoxic activity compared to nOnc and also
XX lower immunogenicity in humans
XX
XX Sequence 355 AA:
SQ
Query Match 97.9%; Score 551; DB 2; Length 355;
Best Local Similarity 97.2%; Pred. No. 4e-36;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DDKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQKPKSPKTIYRANRLVDGVPS 60
DB 1 DDKMTQSPSSMYASIGERVTITCKASQDINSYLSWFOQKPKSPKTIYRANRLVDGVPS 60
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYQYDEPPYFGGTYKLEIK 107
DB 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYQYDEPPYFGGTYKLEIK 107
RESULT 7
AAW35129
ID AAW35129 standard; protein; 355 AA.
XX
XX AAW35129;
AC
XX 20-APR-1998 (first entry)
DT
XX R. pipiens recombinant RNase rOnc fusion protein 5.
DE
XX
XX RNase A; ribonuclease; cytotoxic; oncogene; nOnc; immunofusion;
KM tumour cell growth; frog.
XX
XX Rana pipiens.
OS Synthetic.
XX
XX WO9731116-A2.
XX
XX 28-AUG-1997.
XX
XX 19-FEB-1997; 97WO-US002588.
XX
XX 21-FEB-1996; 96US-0011800P.
XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL, Boque L, Wlodawer A;
 XX
 DR WPI; 1997-435168/40.
 DR N-PSDB; AAT94967.
 XX
 PT Ribonuclease molecules based on native Oncinase - used for killing cells,
 particularly tumour cells.
 XX
 PS Disclosure; Page 71; 90pp; English.
 XX
 CC Sequences AAM35125 to AAM35135 represent recombinant fusion proteins
 CC (rOnc) which are modifications of the RNase Oncinase (RTM) (nOnc). Such
 CC novel ribonuclease molecules are highly cytotoxic and can be used alone
 CC or to form chemical conjugates or to target recombinant immunofusions.
 CC They are used particularly for decreasing tumour cell growth. They can
 CC also be used for cell separation in vitro by selectively killing unwanted
 CC types of cells, e.g. in bone marrow prior to transplantation into a
 CC patient undergoing marrow ablation by radiation, or for killing leukaemia
 CC cells or T-cells that would cause graft versus host disease. The toxins
 CC can also be used to selectively kill unwanted cells in culture. The new
 CC ribonucleases have increased cytotoxic activity compared to nOnc and also
 CC lower immunogenicity in humans
 XX
 SQ Sequence 355 AA;
 Query Match 97.9%; Score 551; DB 2; Length 355;
 Best Local Similarity 97.2%; Pred. No. 4e-36;
 Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIRMTPSSMYASLGERVTITCKASODINSYLSWFOQKPKSKPTLIYRANRLVDGVP 60
 DB 1 DIRMTPSSMYASLGERVTITCKASODINSYLSWFOQKPKSKPTLIYRANRLVDGVP 60
 QY 61 RFGSGSGGDYSLTISLSEYEDMGIIYCYDDEFPYFGGTLEIK 107
 DB 61 RFGSGSGGDYSLTISLSEYEDMGIIYCYDDEFPYFGGTLEIK 107
 RESULT 8
 AAM35127
 ID AAM35127 standard; protein; 358 AA.
 XX
 AC AAM35127;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE R. pipiens recombinant RNase rOnc fusion protein 3.
 XX
 KW RNase A; ribonuclease; cytotoxic; oncinase; nOnc; immunofusion;
 KW tumour cell growth; frog.
 XX
 OS Rana pipiens.
 OS Synthetic.
 OS
 PN WO9731116-A2.
 XX
 PD 28-AUG-1997.
 XX
 PF 19-FEB-1997; 97WO-US002588.
 XX
 PR 21-FEB-1996; 96US-0011800P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL, Boque L, Wlodawer A;
 XX
 DR WPI; 1997-435168/40.
 DR N-PSDB; AAT94965.
 XX
 PT Ribonuclease molecules based on native Oncinase - used for killing cells,
 particularly tumour cells.

XX
 PS Disclosure; Page 69; 90pp; English.
 XX
 CC Sequences AAM35125 to AAM35135 represent recombinant fusion proteins
 CC (rOnc) which are modifications of the RNase Oncinase (RTM) (nOnc). Such
 CC novel ribonuclease molecules are highly cytotoxic and can be used alone
 CC or to form chemical conjugates or to target recombinant immunofusions.
 CC They are used particularly for decreasing tumour cell growth. They can
 CC also be used for cell separation in vitro by selectively killing unwanted
 CC types of cells, e.g. in bone marrow prior to transplantation into a
 CC patient undergoing marrow ablation by radiation, or for killing leukaemia
 CC cells or T-cells that would cause graft versus host disease. The toxins
 CC can also be used to selectively kill unwanted cells in culture. The new
 CC ribonucleases have increased cytotoxic activity compared to nOnc and also
 CC lower immunogenicity in humans
 XX
 SQ Sequence 358 AA;
 Query Match 97.9%; Score 551; DB 2; Length 358;
 Best Local Similarity 97.2%; Pred. No. 4e-36;
 Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DIRMTPSSMYASLGERVTITCKASODINSYLSWFOQKPKSKPTLIYRANRLVDGVP 60
 DB 119 DIRMTPSSMYASLGERVTITCKASODINSYLSWFOQKPKSKPTLIYRANRLVDGVP 178
 QY 61 RFGSGSGGDYSLTISLSEYEDMGIIYCYDDEFPYFGGTLEIK 107
 DB 179 RFGSGSGGDYSLTISLSEYEDMGIIYCYDDEFPYFGGTLEIK 225
 RESULT 9
 AAM35130
 ID AAM35130 standard; protein; 358 AA.
 XX
 AC AAM35130;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE R. pipiens recombinant RNase rOnc fusion protein 6.
 XX
 KW RNase A; ribonuclease; cytotoxic; oncinase; nOnc; immunofusion;
 KW tumour cell growth; frog.
 XX
 OS Rana pipiens.
 OS Synthetic.
 OS
 PN WO9731116-A2.
 XX
 PD 28-AUG-1997.
 XX
 PF 19-FEB-1997; 97WO-US002588.
 XX
 PR 21-FEB-1996; 96US-0011800P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL, Boque L, Wlodawer A;
 XX
 DR WPI; 1997-435168/40.
 DR N-PSDB; AAT94968.
 XX
 PT Ribonuclease molecules based on native Oncinase - used for killing cells,
 particularly tumour cells.
 XX
 PS Disclosure; Page 72; 90pp; English.
 XX
 CC Sequences AAM35125 to AAM35135 represent recombinant fusion proteins
 CC (rOnc) which are modifications of the RNase Oncinase (RTM) (nOnc). Such
 CC novel ribonuclease molecules are highly cytotoxic and can be used alone
 CC or to form chemical conjugates or to target recombinant immunofusions.
 CC They are used particularly for decreasing tumour cell growth. They can
 CC also be used for cell separation in vitro by selectively killing unwanted

CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans
XX
SQ Sequence 358 AA;

Query Match 97.9%; Score 551; DB 2; Length 358;
Best Local Similarity 97.2%; Pred. No. 4e-36;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASLGSRVITTCASQDINSYISWFOQKRGKSPKTLIYRANRLVDGVPS 60
DB 119 DIKMTQSPSSMYASLGSRVITTCASQDINSYISWFOQKRGKSPKTLIYRANRLVDGVPS 178
QY 61 RFGSGSGGDYSLTISLSLEYEDMGIIYCYQYDEFPYTFGGGTRLEIK 107
DB 179 RFGSGSGGDYSLTISLSLEYEDMGIIYCYQYDEFPYTFGGGTRLEIK 225

RESULT 10

AAW35128
ID AAW35128 standard; protein; 360 AA.

XX AAW35128;

DT 20-APR-1998 (first entry)

DE R. pipiens recombinant RNase rOnc fusion protein 4.

KM RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW tumour cell growth; frog.

OS Rana pipiens.
OS Synthetic.

XX WO9731116-A2.

XX 28-AUG-1997.

XX 19-FEB-1997; 97WO-US002588.

XX 21-FEB-1996; 96US-0011800P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rybak SM, Newton DL, Boque L, Wlodawer A;

DR WPI; 1997-435168/40.

DR N-PSDB; AAT94966.

PS Disclosure; Page 70; 90pp; English.

CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
CC or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by transplacation into a
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans

SQ Sequence 360 AA;

Query Match 97.9%; Score 551; DB 2; Length 360;
Best Local Similarity 97.2%; Pred. No. 4.1e-36;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASLGSRVITTCASQDINSYISWFOQKRGKSPKTLIYRANRLVDGVPS 60
DB 121 DIKMTQSPSSMYASLGSRVITTCASQDINSYISWFOQKRGKSPKTLIYRANRLVDGVPS 180
QY 61 RFGSGSGGDYSLTISLSLEYEDMGIIYCYQYDEFPYTFGGGTRLEIK 107
DB 181 RFGSGSGGDYSLTISLSLEYEDMGIIYCYQYDEFPYTFGGGTRLEIK 227

RESULT 11

AAW35126
ID AAW35126 standard; protein; 379 AA.

XX AAW35126;

DT 20-APR-1998 (first entry)

DE R. pipiens recombinant RNase rOnc fusion protein 2.

KM RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW tumour cell growth; frog.

OS Rana pipiens.
OS Synthetic.

XX WO9731116-A2.

XX 28-AUG-1997.

XX 19-FEB-1997; 97WO-US002588.

XX 21-FEB-1996; 96US-0011800P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rybak SM, Newton DL, Boque L, Wlodawer A;

DR WPI; 1997-435168/40.

DR N-PSDB; AAT94964.

PS Disclosure; Page 68; 90pp; English.

CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
CC or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by selectively killing unwanted
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans

SQ Sequence 379 AA;

Query Match 97.9%; Score 551; DB 2; Length 379;
Best Local Similarity 97.2%; Pred. No. 4.3e-36;
Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASLGSRVITTCASQDINSYISWFOQKRGKSPKTLIYRANRLVDGVPS 60
DB 143 DIKMTQSPSSMYASLGSRVITTCASQDINSYISWFOQKRGKSPKTLIYRANRLVDGVPS 202
QY 61 RFGSGSGGDYSLTISLSLEYEDMGIIYCYQYDEFPYTFGGGTRLEIK 107

Db 203 RFSGSGGQDYSLTISLSEYEDMGIIYCYQDFEPYFGGCTKLEIK 249

RESULT 12

AAW27089 ID AAW27089 standard; protein; 214 AA.

XX AAW27089;

AC 18-NOV-1997 (first entry)

XX Mouse monoclonal antibody B9 light chain.

XX Human plasma apolipoprotein B-100; arteriosclerotic lipoprotein;

XX antibody; Fab.

XX Mus musculus.

XX Key Location/Qualifiers

FT Region 24..34

FT Region /label= CDR1

FT Region 50..56

FT Region /label= CDR2

FT Region 89..97

FT Region /label= CDR3

FT Region 108..214

FT Region /label= Ckappa

XX JPO9154587-A.

XX 17-JUN-1997.

XX 09-MAY-1996; 96JP-00114492.

XX 02-NOV-1995; 95KR-00039459.

XX (KOAD) KOREAN SCI & TECHNOLOGY RES CENT.

XX WPI; 1997-367067/34.

XX N-PSDB; AAT85091.

XX DNA encoding mouse antibody binding human plasma apo-lipoprotein B-100 -

XX useful for removing arteriosclerotic lipoprotein(s).

XX Claim 4; Fig 6; 17pp; Japanese.

XX The present sequence represents the mouse monoclonal antibody B9 light

XX chain (B9L), which binds specifically to human blood apolipoprotein B-

XX 100. The nucleic acid can be used in a method for the preparation of a

XX recombinant antibody which specifically binds human plasma

XX apolipoprotein B-100. The antibody can be used as a reagent for

XX determining the concentration of human plasma apolipoprotein B-100 in a

XX sample. The antibody is also useful in a drug composition for selectively

XX removing arteriosclerotic lipoproteins containing human plasma

XX apolipoprotein B-100

XX Sequence 214 AA;

XX Query Match 97.3%; Score 548; DB 2; Length 214;

XX Best Local Similarity 97.2%; Pred. No. 4.3e-36;

XX Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

AAR95946 ID AAR95946 standard; protein; 127 AA.

XX AAR95946;

XX 10-FEB-1997 (first entry)

XX HNK-20 variable kappa chain.

XX Antibody; HNK-20; variable kappa chain; hybridoma; murine; IgA; mouse;

XX F glycoprotein; respiratory syncytial virus; RSV; constant region gene;

XX chimeric antibody; isotype-switched antibody; therapy; infection; human;

XX pneumonia; bronchiolitis; animal.

XX Mus musculus.

XX WO9616974-A1.

XX 06-JUN-1996.

XX 01-DEC-1995; 95WO-US015716.

XX 01-DEC-1994; 94US-00348548.

XX (ORAV-) ORAVAX INC.

XX Berdoz J, Kraehenbuhl J;

XX WPI; 1996-286826/29.

XX N-PSDB; AAT30456.

XX DNA encoding variable region of antibody HNK-20 - for treating

XX respiratory syncytial virus infection.

XX Claim 9; Page 30; 75pp; English.

XX AAR95946-R95948 represent sequences for variable regions of an antibody

XX produced by the hybridoma cell line HNK-20. This sequence represents the

XX sequence for the antibody HNK-20 variable kappa chain. HNK-20 is a murine

XX hybridoma cell line, that produces IgA specific for the F glycoprotein of

XX respiratory syncytial virus (RSV). The DNA encoding these sequences were

XX isolated using primers specific for the 5' untranslated region of the

XX variable region, and for the intron downstream of the rearranged J region

XX (see AAT30459-310545 for primer sequences). The DNA encoding these

XX sequences can be inserted into vectors containing heterologous (such as

XX human) constant region genes, for the production of chimeric and isotype-

XX switched antibodies. The antibodies are useful in the treatment and

XX diagnosis of infection by RSV, such as pneumonia and bronchiolitis, in

XX humans and animals. By using genomic DNA as a template, variable region

XX genes can be isolated without producing fragments that have to be adapted

XX for recombinant antibody expression. Also, by using the genomic DNA, no

XX knowledge of the DNA sequence encoding the target variable region is

XX required. Chimeric antibodies produced from these proteins, that contain

XX the constant region of the host being treated, are less likely to cause

XX adverse immune reactions

XX Sequence 127 AA;

XX Query Match 97.0%; Score 546; DB 2; Length 127;

XX Best Local Similarity 95.3%; Pred. No. 3.7e-36;

XX Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

AAR95946 ID AAR95946 standard; protein; 127 AA.

XX AAR95946;

XX 10-FEB-1997 (first entry)

XX HNK-20 variable kappa chain.

XX Antibody; HNK-20; variable kappa chain; hybridoma; murine; IgA; mouse;

XX F glycoprotein; respiratory syncytial virus; RSV; constant region gene;

XX chimeric antibody; isotype-switched antibody; therapy; infection; human;

XX pneumonia; bronchiolitis; animal.

XX Mus musculus.

XX WO9616974-A1.

XX 06-JUN-1996.

XX 01-DEC-1995; 95WO-US015716.

XX 01-DEC-1994; 94US-00348548.

XX (ORAV-) ORAVAX INC.

XX Berdoz J, Kraehenbuhl J;

XX WPI; 1996-286826/29.

XX N-PSDB; AAT30456.

XX DNA encoding variable region of antibody HNK-20 - for treating

XX respiratory syncytial virus infection.

XX Claim 9; Page 30; 75pp; English.

XX AAR95946-R95948 represent sequences for variable regions of an antibody

XX produced by the hybridoma cell line HNK-20. This sequence represents the

XX sequence for the antibody HNK-20 variable kappa chain. HNK-20 is a murine

XX hybridoma cell line, that produces IgA specific for the F glycoprotein of

XX respiratory syncytial virus (RSV). The DNA encoding these sequences were

XX isolated using primers specific for the 5' untranslated region of the

XX variable region, and for the intron downstream of the rearranged J region

XX (see AAT30459-310545 for primer sequences). The DNA encoding these

XX sequences can be inserted into vectors containing heterologous (such as

XX human) constant region genes, for the production of chimeric and isotype-

XX switched antibodies. The antibodies are useful in the treatment and

XX diagnosis of infection by RSV, such as pneumonia and bronchiolitis, in

XX humans and animals. By using genomic DNA as a template, variable region

XX genes can be isolated without producing fragments that have to be adapted

XX for recombinant antibody expression. Also, by using the genomic DNA, no

XX knowledge of the DNA sequence encoding the target variable region is

XX required. Chimeric antibodies produced from these proteins, that contain

XX the constant region of the host being treated, are less likely to cause

XX adverse immune reactions

XX Sequence 127 AA;

XX Query Match 97.0%; Score 546; DB 2; Length 127;

XX Best Local Similarity 95.3%; Pred. No. 3.7e-36;

XX Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

RESULT 14

AAB86037

ID AAB6037 standard; protein; 246 AA.
 XX AAB6037;
 AC
 XX 16-JUL-2001 (first entry)
 DT
 XX Murine anti-CA19-9 antigen protein.
 DE
 XX Antigen; CA19-9; murine; variable heavy chain; VH; anti-CA19-9; cancer;
 KM variable light chain; VL; cytototoxic; detection; stomach tumor cell;
 KM pancreas tumor cell; immunotherapy; single-chain Fv; drug targeting;
 KM produg activation.
 XX
 OS Mus sp.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Domain 5..113
 FT /label= VH
 FT Region 114..144
 FT /note= "Linker segment"
 FT Domain 145..244
 FT /label= VL
 PN
 XX EPI090927-A1.
 PD
 XX 11-APR-2001.
 PF 08-OCT-1999; 99EP-00120119.
 PR 08-OCT-1999; 99EP-00120119.
 XX (ABKE/) ABKEN H.
 XX
 PI Abken H;
 DR WPI; 2001-345810/37.
 DR N-PSDB; AAF88024.
 XX
 PT New single-chain Fv fragment specific for antigen CA19-9, useful for
 PT diagnosis and treatment of tumors, particularly of stomach and pancreas.
 XX
 PS Claim 6; Fig 1; 23pp; German.
 XX
 CC This invention describes a novel polypeptide (I), comprising an
 CC oligopeptide (OP1) having the variable region of the heavy chain (VH) of
 CC an anti-CA19-9 antibody (Ab), or its fragment with the same binding
 CC specificity for CA19-9 antigen, and an oligopeptide (OP2) based on the
 CC variable light chain (VL) region of an Ab, or its fragment, is new. OP1
 CC and OP2 are linked, directly or through a linker peptide (LP). The
 CC products of the invention have cytotoxic activity. (I), optionally in
 CC pharmaceutical form or fused to other active substances, is used as
 CC an elimination agent for detection, localization and/or
 CC pharmacological or diagnostic agent for detection, localization and/or
 CC elimination of cells that express the CA19-9 antigen, especially stomach
 CC or pancreas tumor cells. When linked to other binding domains, (I) can be
 CC used to produce bi- or multi-specific antibodies, also useful for
 CC immunotherapy of cancers. (I), a single-chain Fv fragment, has good
 CC solubility in water, is renatured to active form very efficiently after
 CC denaturation, penetrates tissue well, and accumulates on CA19-9-
 CC presenting cells in vivo, but not on normal cells. (I) is not
 CC internalized by the cells, and has a long residence time on the cell
 CC surface, without degradation by cytoplasmic processes, making it well
 CC suited for drug targeting, or produg activation. Since (I) do not
 CC include murine constant regions, it should be possible to administer them
 CC repeatedly without inducing a human anti-murine antibody response. Also,
 CC when coupled to the human CH2CH3 immunoglobulin domains, they cause
 CC specific lysis of tumor cells. This sequence represents the mouse derived
 CC anti-CA19-9 antibody construct described in the method of the invention
 CC
 XX
 SO Sequence 246 AA;
 Query Match 97.0%; Score 546; DB 4; Length 246;
 Best Local Similarity 97.2%; Pred. No. 7e-36;

Matches 104; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DDKMTGSPSSMTVASLGERVITTCASODINSYLSWFQKRGKSPKTLIRANRLVDGVS 60
 DB 137 DDKMTGSPSSMTVASLGERVITTCASODINSYLSWFQKRGKSPKTLIRANRLVDGVS 196
 QY 61 RFGSGSGGQDYSLTISLSEYEDMGIIYCYQYDEFPPTFGGTRLEIK 107
 DB 197 RFGSGSGGQDYSLTISLSEYEDMGIIYCYQYDEFPPTFGGTRLEIK 243
 RESULT 15
 ID AAM58505 standard; protein; 107 AA.
 XX AAM58505;
 AC
 XX 18-AUG-1998 (first entry)
 DT
 XX H65 protein sequence SEQ ID NO:26 from Fig 6.
 DE
 XX Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
 KM depletion; cytotoxic; immunocytotoxic; fusion protein; psoriasis;
 KM autoimmune disease; rheumatoid arthritis; type I diabetes.
 XX
 OS Mus sp.
 XX
 EN US5770196-A.
 XX
 PD 23-JUN-1998.
 PF 07-JUN-1995; 95US-004727288.
 PR 13-DEC-1991; 91US-00808464.
 PR 14-DEC-1992; 92WO-US010906.
 PR 23-JUN-1993; 93US-00082842.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Studnicka GM;
 DR WPI; 1998-376744/32.
 XX
 PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies with
 PT humanised variable regions.
 XX
 PS Example 6; Col 61-64; 77pp; English.
 XX
 CC A method has been developed of depleting CD5+ cells in an animal. The
 CC method comprises administering a cytotoxic protein containing a modified
 CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
 CC molecule or an immunocytotoxic or fusion protein containing an anti-CD5
 CC Ig molecule, and where the modified Ig variable domain comprises at least
 CC one of (a) a modified light chain variable region (see AAM58478 or
 CC AAM58480), and (b) a modified heavy chain variable region (see AAM58479
 CC or AAM58481), where AAM58478 and AAM58479 are humanised forms of the H65
 CC light and heavy chain variable domains with low risk amino acid
 CC substitutions [i.e. low risk of reducing antigen-binding specificity.]
 CC and AAM58480 and AAM58481 are humanised forms of the H65 light and heavy
 CC chain variable domains with moderate risk amino acid substitutions and
 CC are present in humanised H65 antibody h63 (ATCC HB 11206). The method is
 CC useful for treating autoimmune diseases, especially systemic lupus
 CC erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The
 CC present sequence represents an H65 sequence from the present invention
 CC
 XX
 SO Sequence 107 AA;
 Query Match 96.1%; Score 541; DB 2; Length 107;
 Best Local Similarity 96.3%; Pred. No. 7.9e-36;
 Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DDKMTGSPSSMTVASLGERVITTCASODINSYLSWFQKRGKSPKTLIRANRLVDGVS 60
 |||

Db 1 DIRMTPSSMVASIGERVITCKASODINSYLSPFOOKPGKSPKTLIRANRLVDGVP 60
QY 61 RFGSGSGGQDYSLTISLIEYEDMGIIYYCLOYDERPPTFGGKLEIK 107
Db 61 RFGSGSGGQDYSLTISLIEYEDMGIIYYCLOYDERPPTFGGKLEIK 107

Search completed: December 29, 2004, 17:57:26
Job time : 76.5428 secs

THIS PAGE BLANK (USE P. 79)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:38:43 ; Search time 73.8584 Seconds
(without alignments)
833.556 Million cell updates/sec

Title: US-10-774-076-3

Perfect score: 563
Sequence: 1 DIRMTPSSMYASISGERVT.....CLOYDEPPTFGGTLEIK 107

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	98.4	236	2 Q7TS98	Q7TS98 mus musculu
2	546	97.0	214	2 Q9RIAS	Q9RIAS mus musculu
3	534	94.8	128	1 KV5E_MOUSE	P01637 mus musculu
4	499	88.6	115	1 KV5F_MOUSE	P01638 mus musculu
5	468	83.1	236	2 Q7TMK3	Q7TMK3 mus musculu
6	398	70.7	108	1 KV1Y_HUMAN	P80362 homo sapien
7	394	70.0	108	1 KV1O_HUMAN	P01607 homo sapien
8	394	70.0	236	2 Q7Z3Y4	Q7Z3Y4 homo sapien
9	393	69.8	108	1 KV1B_HUMAN	P01594 homo sapien
10	392	69.6	108	2 Q9UL70	Q9UL70 homo sapien
11	391	69.4	108	1 KV1P_HUMAN	P01608 homo sapien
12	389	69.1	236	2 Q6GMK8	Q6GMK8 homo sapien
13	388	68.9	108	1 KV1V_HUMAN	P04430 homo sapien
14	384	68.2	236	2 Q6GMK9	Q6GMK9 homo sapien
15	383	68.0	108	1 KV1R_HUMAN	P01593 homo sapien
16	382	67.9	108	1 KV1A_HUMAN	P01593 homo sapien
17	382	67.9	108	1 KV1L_HUMAN	P01605 homo sapien
18	382	67.9	108	1 KV5O_MOUSE	P01648 mus musculu
19	381	67.7	108	1 KV1O_HUMAN	P01609 homo sapien
20	380	67.5	108	1 KV5T_MOUSE	P01653 mus musculu
21	379	67.3	108	1 KV5S_MOUSE	P01652 mus musculu
22	379	67.3	298	2 Q9QYFO	Q9QYFO synthe c
23	378.5	67.2	107	2 Q96SA9	Q96SA9 mus musculu
24	378	67.1	109	2 Q920B6	Q920B6 mus musculu
25	377	67.0	236	2 Q6PIH7	Q6PIH7 homo sapien
26	377	67.0	236	2 Q6GMW1	Q6GMW1 homo sapien
27	377	67.0	236	2 AAH34141	AAH34141 homo sapi
28	376	66.8	108	1 KV1M_HUMAN	P01647 mus musculu
29	376	66.8	108	1 KV5N_MOUSE	P01650 mus musculu
30	376	66.8	108	1 KV5Q_MOUSE	Q6GMX0 homo sapien
31	376	66.8	236	2 Q6GMX0	Q6GMX0 homo sapien

32	375	66.6	108	2 Q9UL77	Q9UL77 homo sapien
33	374	66.4	108	1 KV1H_HUMAN	P01600 homo sapien
34	374	66.4	108	1 KV5K_MOUSE	P01644 mus musculu
35	374	66.4	111	2 AAR10992	AAR10992 mus muscu
36	373.5	66.3	107	1 KV1D_HUMAN	P01596 homo sapien
37	373	66.3	234	2 Q7Z473	Q7Z473 homo sapien
38	372	66.1	108	1 KV5L_MOUSE	P01645 mus musculu
39	371.5	66.0	112	2 Q8X1F3	Q8X1F3 mus musculu
40	371	65.9	108	1 KV1C_HUMAN	P01595 homo sapien
41	371	65.9	108	1 KV5M_MOUSE	P01646 mus musculu
42	371	65.9	108	2 Q9UL79	Q9UL79 homo sapien
43	370	65.7	108	1 KV5P_MOUSE	P01649 mus musculu
44	370	65.7	130	1 KV5G_MOUSE	P01639 mus musculu
45	370	65.7	234	2 Q8R062	Q8R062 mus musculu

ALIGNMENTS

RESULT 1

Q7TS98	PRELIMINARY;	PRT;	236 AA.
AC Q7TS98;			
DT 01-OCT-2003 (TREMBlrel. 25, Created)			
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)			
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
DE Anti-colorectal carcinoma light chain.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RF SEQUENCE FROM N.A.			
RX MEDLINE=93363497; PubMed=8372513;			
RA Tonge D.W., Henham J.F., Greene A.R., Lee I.D., Edge M.D.;			
RT "Cloning and characterization of 116S19.9 heavy and light chain cDNAs and expression of antibody fragments in Escherichia coli.";			
RL Year Immunol. 7:56-62(1993).			
DR EMBL; S65921; AAB28160.1; -			
DR InterPro; IPR007110; IG_1ike.			
DR InterPro; IPR003597; IG_C1.			
DR InterPro; IPR003006; IG_MHC.			
DR InterPro; IPR003596; IG_V.			
DR Pfam; PF00654; C1-sect; 1.			
DR Pfam; PF00647; Ig; 1.			
DR SMART; SM00406; IgV; 1.			
DR PROSITE; PS00835; IG_LIKE; 2.			
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.			
SQ SEQUENCE 236 AA, 26454 MW, 2C56EBB5EA10F4C CRC64;			
Query Match	98.4%;	Score 554;	DB 2; Length 236;
Best Local Similarity	99.1%;	Pred. No. 1.9e-49;	
Matches 106;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
QY 1 DIRMTPSSMYASISGERVTITCKASODINSYISWFOQKRGSKPKTLIVRANLVQVPS 60			
DB 23 DIRMTPSSMYASISGERVTITCKASODINSYISWFOQKRGSKPKTLIVRANLVQVPS 82			
QY 61 RFSGSGSGDYSLTISLSLEYEDMGIIYVCLQYDFPPTFGGTTLEIK 107			
DB 83 RFSGSGSGDYSLTISLSLEYEDMGIIYVCLQYDFPPTFGGTTLEIK 129			
RESULT 2			
Q9RIAS	PRELIMINARY;	PRT;	214 AA.
AC Q9RIAS;			
DT 01-MAY-2000 (TREMBlrel. 13, Created)			
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)			
DE Kappa light chain of Mab7 (Fragment).			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA White K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF152371; AAD40242.1; -
 DR PIR; PH1065; PH1065.
 DR PDB; 1AHM; X-ray; D=-.
 DR PDB; 1CIC; X-ray; A/C=1-214.
 DR PDB; 1E08; X-ray; -
 DR PDB; 1K6Q; X-ray; L=1-210.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig CL.
 DR InterPro; IPR003066; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF07654; C1-set; 1.
 DR Pfam; PF00047; Ig; 1.
 DR PRINTS; PRO0024; HOMEBOX.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1 1
 FT 214 214
 SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE95F2A CRC64;
 Query Match 97.0%; Score 546; DB 2; Length 214;
 Best Local Similarity 96.3%; Pred. No. 1.2e-48;
 Matches 103; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIRMTPSSSMYASLGERVTITCKASQDINSYLSFPOKRGKSPKTLRYRANRLVDGVPS 60
 DB 1 DIRMTPSSSMYASLGERVTITCKASQDINSYLSFPOKRGKSPKTLRYRANRLVDGVPS 60
 QY 61 RFSGSGSGDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGKLEIK 107
 DB 61 RFSGSGSGDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGKLEIK 107
 RESULT 3
 KVSE MOUSE STANDARD; PRT; 128 AA.
 ID KVSE MOUSE P01637;
 AC P01637;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region T1 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=81052342; PubMed=6776411;
 RA Altenburger W., Steinmetz M., Zachau H.G.;
 RT "Functional and non-functional joining in immunoglobulin light chain
 genes of a mouse myeloma";
 RL Nature 287:603-607(1980).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 DR EMBL; V00772; CAA24150.1; -
 DR PIR; A01920; KMWSTL.

DR HSSP; P80362; 1MTU.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT CHAIN 1 20
 FT SIGNAL 20
 FT DOMAIN 21 128 Ig kappa chain V-V region T1.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 54 Complementarity-determining-1.
 FT DOMAIN 55 69 Framework-2.
 FT DOMAIN 70 76 Complementarity-determining-2.
 FT DOMAIN 77 108 Framework-3.
 FT DOMAIN 109 117 Complementarity-determining-3.
 FT DOMAIN 118 127 Framework-4.
 FT DISULFID 43 108 By similarity.
 FT NON_TER 128 128
 SQ SEQUENCE 128 AA; 14385 MW; AFA569031BB7E05 CRC64;

Query Match 94.8%; Score 534; DB 1; Length 128;
 Best Local Similarity 93.5%; Pred. No. 1.2e-47;
 Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIRMTPSSSMYASLGERVTITCKASQDINSYLSFPOKRGKSPKTLRYRANRLVDGVPS 60
 DB 21 DIRMTPSSSMYASLGERVTITCKASQDINSYLSFPOKRGKSPKTLRYRANRLVDGVPS 80
 QY 61 RFSGSGSGDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGKLEIK 107
 DB 81 RFSGSGSGDYSLTISLSEYEDMGIIYCYQYDEFPYTFGGGKLEIK 127

RESULT 4
 KVSE MOUSE STANDARD; PRT; 115 AA.
 ID KVSE MOUSE P01638;
 AC P01638;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region L6 precursor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=81220975; PubMed=6264318;
 RA Pech M., Hochl J., Schnell H., Zachau H.G.;
 RT "Differences between germ-line and rearranged immunoglobulin V kappa
 RT coding sequences suggest a localized mutation mechanism";
 RL Nature 291:668-670(1981).
 DR PIR; A01921; KMWSTL.
 DR HSSP; P01607; 1BWW.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT CHAIN 1 20
 FT SIGNAL 20
 FT DOMAIN 21 115 Ig kappa chain V-V region L6.
 FT DOMAIN 21 43 Framework-1.
 FT DOMAIN 44 54 Complementarity-determining-1.
 FT DOMAIN 55 69 Framework-2.
 FT DOMAIN 70 76 Complementarity-determining-2.
 FT DOMAIN 77 108 Framework-3.
 FT DOMAIN 109 115 Complementarity-determining-3.
 FT DISULFID 43 108 By similarity.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12986 MW; BA852C58F328E1C3 CRC64;
 Query Match 88.6%; Score 499; DB 1; Length 115;

Best Local Similarity 100.0%; Pred. No. 4.5e-44;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDKTOSPPSSMYASLGERVITTCASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
Db 21 DDKTOSPPSSMYASLGERVITTCASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 80

QY 61 RFGSGSGGDYSLTSSLEVEDMGITYCLOYDEPP 95
Db 81 RFGSGSGGDYSLTSSLEVEDMGITYCLOYDEPP 115

RESULT 5

07TMK3 PRELIMINARY; PRT; 236 AA.
AC 07TMK3
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatzenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Cammioni P., Prange C.,
RA Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalitz D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Strauberg R.;
RL Submitted (JUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL, BC055906, AAHS5906.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; Cl-sec; I.
DR Pfam: PF00047; Ig; I.
DR SMART: SM00406; IgV; I.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 236 AA; 26299 MW; 0DB03488AA6396F CRC64;

Query Match 83.1%; Score 468; DB 2; Length 236;
Best Local Similarity 85.0%; Pred. No. 1.8e-40;
Matches 91; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 1 DDKTOSPPSSMYASLGERVITTCASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60

Db 23 DDKTOSPPSSMYASLGERVITTCASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 82

QY 61 RFGSGSGGDYSLTSSLEVEDMGITYCLOYDEPPYFGGTLEIK 107
Db 83 RFGSGSGGDYSLTSSLEVEDMGITYCLOYDEPPYFGGTLEIK 129

RESULT 6

KVLY HUMAN STANDARD; PRT; 108 AA.
ID KVLY HUMAN
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-1 region VAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=793911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eultz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).

RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Var.";
RL J. Mol. Biol. 147:185-193(1981).

CC 1-1 MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB: 1WTV; X-ray; A/B=1-108.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR003596; Ig-like.
DR InterPro: IPR007110; Ig_v.
DR Pfam: PF00047; Ig; I.
DR SMART: SM00406; IgV; I.
DR PROSITE: PS50835; IG_LIKE; 1.
KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT STRAND 30 31 TN -> SD (in Ref. 2).
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT STRAND 40 41
FT STRAND 45 49
FT STRAND 50 52
FT STRAND 53 54
FT STRAND 56 57
FT STRAND 60 61
FT STRAND 62 67
FT STRAND 68 69
FT STRAND 70 75

```

FT HELIX 80 82
FT STRAND 84 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match
Best Local Similarity 70.7%; Score 398; DB 1; Length 108;
Matches 73; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

QY 1 D1KMTQSPSSMYASIGERTVITCKASQDINSYLSWFOQPKSPKTLTYRANRLVDGVPS 60
D 1 D1QMTQSPSSLSASVDKRVITTCRASQDITNTVMNFPQRPQAPKVLITGASILETVPS 60
QY 61 RFGSGSGGSDYSLTISLSEYEDMGIIYCLQYDEFPYTGSGTKLEIK 107
D 61 RFGSGSGGSDYSLTISLSEYEDMGIIYCLQYDEFPYTGSGTKLEIK 107

RESULT 7
KV10 HUMAN STANDARD; PRT; 108 AA.
ID KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-1 region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RA MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein RSI refined at 2.0-A resolution."
RL Biochemistry 14:4943-4952 (1975).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A9163; KIHURE.
DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BMW; X-ray; A/B=1-107.
DR PDB; 1REI; X-ray; A/B=1-107.
DR GO; GO:0005573; C:extracellular; NAS.
DR GO; GO:0003923; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SMO0406; IgV; 1.
DR SMART; SMO0407; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KM 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.

```

```

FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT TURN 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match
Best Local Similarity 70.0%; Score 394; DB 1; Length 108;
Matches 74; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 D1KMTQSPSSMYASIGERTVITCKASQDINSYLSWFOQPKSPKTLTYRANRLVDGVPS 60
D 1 D1QMTQSPSSLSASVDKRVITTCRASQDITNTVMNFPQRPQAPKVLITGASILETVPS 60
QY 61 RFGSGSGGSDYSLTISLSEYEDMGIIYCLQYDEFPYTGSGTKLEIK 106
D 61 RFGSGSGGSDYSLTISLSEYEDMGIIYCLQYDEFPYTGSGTKLEIK 106

RESULT 8
ID 0723Y4 PRELIMINARY; PRT; 236 AA.
AC 0723Y4;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sketelal Muscle;
RX MEDLINE=22386257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abreson R.D., Mullaly S.J.,
RA Bosak S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

```

```

[2]
SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Straubeberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
DR InterPro; IPR007110; Ig-1-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ
SEQUENCE 236 AA; 25702 MW; 7F8F84BD23084BC6 CRC64;

Query Match 70.0%; Score 394; DB 2; Length 236;
Best Local Similarity 69.2%; Pred. No. 9e-33;
Matches 74; Conservative 16; Mismatches 17; Indels 0; Gaps 0

OY 1 DIKMTQSSSSMYASGERTYITCKRSQDINSYLSWFOOKPQKSPKTLIYRANRLVDGYPS 60
DB 23 DIQMTQSSSSLASASGDTYITCKRSQDINSYLAIFQOKPQKAPKSLIYGASSLSQSGVOS 82
OY 61 RPSGSGSGQDYSLTITSSLEBEDMGIIYCYCLQYDEPFYRGGGTKEIK 107
DB 83 RFGSGSGGTDFLTITSSIQPEDFANYTCQYKSYPTVYGGGTKEIK 129

RESULT 9
KVLB_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-1 region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fellhammer H., Schiffer M., Epp O., Colman P.M., Iatman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
RN [3]
RP MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91653; K1RH0AU.
DR PDB; 1UV5; X-RAY; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-1-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

```

DR	PROSITE	PS50835; IG_LIKE; 1.	3D-structure; Bence-Jones protein; Direct protein sequencing;
KM	Immunoglobulin V region.		
FT	DOMAIN	1	23
FT	DOMAIN	24	34
FT	DOMAIN	35	49
FT	DOMAIN	50	56
FT	DOMAIN	57	88
FT	DOMAIN	89	97
FT	DOMAIN	98	107
FT	DISULFID	23	88
FT	STRAND	4	5
FT	STRAND	10	13
FT	STRAND	15	16
FT	STRAND	19	25
FT	STRAND	30	31
FT	STRAND	33	38
FT	STRAND	40	41
FT	STRAND	44	49
FT	TURN	50	52
FT	TURN	53	54
FT	TURN	56	57
FT	TURN	60	61
FT	STRAND	62	67
FT	TURN	68	69
FT	STRAND	70	75
FT	HELIx	80	82
FT	STRAND	85	90
FT	STRAND	97	98
FT	STRAND	102	106
FT	NON TER	108	108
SQ	SEQUENCE	108 AA; 11939 MW; E801187B6F67B9 CRC64;	
Query Match		69.8%; Score 393; DB 1; Length 108;	
Best Local Similarity		68.2%; Pred. No. 4,7e-33;	
Matches	73; Conservative	16; Mismatches	18; Indels 0; Gaps
Qy	1	DIKKTQSPSSMYASLGERVTITCKASQDINSYISWFQKRGKSPKTLIYRANRLVDGVS	60
Db	1	DIQMTQSPSSLASVSGRVITTCQASQDISDYINMYQKRGKAPKLLIYDASNLSEGVPS	60
Qy	61	RFSGSGCGDYSLTISLSLEYEDNGIYYCYQYDEFPYTPGGGKTKLEIK	107
Db	61	RFSGSGGAFPTFTISLSLOPEDIATYYCOQYDYLPTWTFQGTQVBEIK	107

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 FT NON_TER 1
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11633 MW; B7BEDCB4FCCA37 CRC64;

Query Match 69.4%; Score 392; DB 2; Length 108;
 Best Local Similarity 69.2%; Pred. No. 5.9e-33;
 Matches 74; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASLGERTVITCKASODINSYLSMFQKRGKSPKTLIYRANRLVDGVPS 60
 DB 1 DIKMTQSPSSLSASVSDRVITTCRASOGISNYLAWYQKRGKVPKSLIYASTLQSGVPS 60
 QY 61 RFGSGSGGDYSLTISLSEYEDMGIYCYQYDEFPYTFGGTKLEIK 107
 DB 61 RFGSGSGGTDFTLTISLTQPEDVATYYCCKNKSARTRTPGKLEIK 107

RESULT 11

ID KVI1P_HUMAN STANDARD; PRT; 108 AA.

AC P01608;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 05-JUL-2004 (rel. 44, Last annotation update)
 DE IG kappa chain V-I region Roy.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=68362076; PubMed=5595110;
 RA Hilechmann N.;
 RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.)";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
 RN [2]
 RP REVISIONS TO 39 AND 41.
 RA Hilechmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
 RA Steinmetz-Kayne M., Suter L., Watanabe S.;
 RL (in) Franek F., Shugar D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR HSSP; P01607; 1BWV.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 1.
 KW Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DISULFID 98 107 Framework-4.
 FT NON_TER 23 88 By similarity.
 SQ SEQUENCE 108 AA; 11782 MW; FSACBDE5A33DFA CRC64;

Query Match 69.4%; Score 391; DB 1; Length 108;
 Best Local Similarity 66.4%; Pred. No. 7.5e-33;

Matches 71; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASLGERTVITCKASODINSYLSMFQKRGKSPKTLIYRANRLVDGVPS 60
 DB 1 DIKMTQSPSSLSASVSDRVITTCRASOGISNYLAWYQKRGKVPKSLIYASTLQSGVPS 60
 QY 61 RFGSGSGGDYSLTISLSEYEDMGIYCYQYDEFPYTFGGTKLEIK 107
 DB 61 RFGSGSGGTDFTLTISLTQPEDVATYYCCKNKSARTRTPGKLEIK 107

RESULT 12

ID O6GMX8 PRELIMINARY; PRT; 236 AA.

AC O6GMX8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheimen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.D., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullanb S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073764; AAH73764.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00654; CI-set; 1.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG LIKE; 2.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein; UNKNOWN_1.
 SQ SEQUENCE 236 AA; 25707 MW; 4FCB814B6559EFC9 CRC64;

Query Match 69.4%; Score 389; DB 2; Length 236;
 Best Local Similarity 68.2%; Pred. No. 3e-32;
 Matches 73; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASLGERTVITCKASODINSYLSMFQKRGKSPKTLIYRANRLVDGVPS 60

```
Db 23 D1QMTQSPSSVSASVGRVITTCRASQGISSTWLAAYQKPKAPRLILYAASSTLSQSVPS 82
QY 61 RFSSSGSGQDYSLTISLSEYEDMGIIYCLQYDEPPYFGGTTKLEIK 107
Db 83 RFSSSGSGTDFLTISLQPEDFATYYCOQAHSPFPPTGPGTKVDIK 129

RESULT 13
KVIR_HUMAN STANDARD; PRT; 108 AA.
AC 06GMK9;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 05-JUL-2004 (Rel. 44, last annotation update)
DE IG kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwyler F.E.; O'Connor T.P.; Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR HSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 2 34 Complementarity-determining-1.
FT DOMAIN 3 49 Framework-2.
FT DOMAIN 4 56 Complementarity-determining-2.
FT DOMAIN 5 57 Framework-3.
FT DOMAIN 6 88 Framework-4.
FT DOMAIN 7 97 Complementarity-determining-3.
FT DISULFID 98 107 Framework-4.
FT NON_TER 23 88 By similarity.
SQ SEQUENCE 108 AA; 11840 MM; CD3PD44FE96FD37 CRC64;

Query Match 68.9%; Score 388; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 1.5e-32;
Matches 70; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

QY 1 D1KMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKPTLIYRANRLVDGVP 60
Db 1 D1QMTQSPSSLSASVGRVITTCRASQSVYNYVAMPQKPKAKSLIYASTLSQSVPS 60
QY 61 RFSSSGSGQDYSLTISLSEYEDMGIIYCLQYDEPPYFGGTTKLEIK 107
Db 61 RFSSSGSGTDFLTISLQPEDFATYYCOQAHSPFPPTGPGTKVDIK 107

RESULT 14
06GMK9 PRELIMINARY; PRT; 236 AA.
AC 06GMK9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
```

```
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Datchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Donald M.F.; Casavant T.L.; Scheetz T.B.;
RA Brownstein M.J.; Udell T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Bosak S.A.; McGwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Wotley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahy J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Kravinsky M.I.; Skolnik A.; Smalios D.E.; Schnerch A.; Schein J.E.;
RA Jones S.U.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RX EMBL; BC073763; AAH73763.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003506; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00654; Cl-set; 1.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MM; FDE2039DC560CF7 CRC64;

Query Match 68.2%; Score 384; DB 2; Length 236;
Best Local Similarity 65.4%; Pred. No. 9.9e-32;
Matches 70; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

QY 1 D1KMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKPTLIYRANRLVDGVP 60
Db 23 D1QMTQSPSSLSASVGRVITTCRASQSVYNYVAMPQKPKAKSLIYASTLSQSVPS 82
QY 61 RFSSSGSGQDYSLTISLSEYEDMGIIYCLQYDEPPYFGGTTKLEIK 107
Db 83 RFSSSGSGTDFLTISLQPEDFATYYCOQAHSPFPPTGPGTKVDIK 129

RESULT 15
KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 05-JUL-2004 (Rel. 44, last annotation update)
DE IG kappa chain V-I region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
```

RA Gon1 F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IgM
 RT (protein WEA) with antibody activity against 3,4-pyruvylated galactose
 RT in Klebsiella polysaccharides K30 and K33.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 CC -1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
 CC against 3,4-pyruvylated galactose and isolated from a patient with
 CC Waldenström's macroglobulinemia.
 DR PIR; A01876; KIHWE.
 DR HSSP; P80362; 1WTU.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region;
 KW Monoclonal antibody.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA, 11840 MW, 9249B61F0945618C CRC64;

Query Match 68.0%; Score 383; DB 1; Length 108;
 Best Local Similarity 66.4%; Pred. No. 5.1e-32;
 Matches 71; Conservative 17; Mismatches 19; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSMFQOKPKSPKTLIYRANRLVDGVP 60
 DB 1 DIKMTQSPSSLSASVGDVNTITCKRASQGRINDLTWYQOKPGTAPKRLIYGATSLQSGVPS 60
 QY 61 RFSGSGSQDYLITISLSEYEDMGIVYCLQYDEFPYTFGGGTKLEIK 107
 DB 61 RFSGSGSGTEFTLTINSIQPEDPATYVCLQYSSSFPWTGGQTKVEVK 107

Search completed: December 29, 2004, 18:05:18
 Job time : 75.8584 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 14.677 Seconds
(without alignments)
701.451 Million cell updates/sec

Title: US-10-774-076-3

Perfect score: 563

Sequence: 1 DIKWTQSPSSMYASLSGERVT.....CLOYDEPPTFGGTTKLEIK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546	97.0	127	2 S52447	Ig kappa chain V r
2	534	94.8	128	1 KVMST1	Ig kappa chain pre
3	525	93.3	234	2 S14237	Ig kappa chain pre
4	519	92.2	128	2 PLO101	Ig kappa chain pre
5	506	89.9	106	2 S20652	Ig kappa chain V r
6	499	86.6	115	1 KYMSR6	Ig kappa chain pre
7	487	86.5	98	2 PHI065	Ig kappa chain V r
8	460	81.7	104	2 S13700	Ig kappa chain V r
9	440	78.2	103	2 S13703	Ig kappa chain V r
10	412	73.2	129	2 B23986	Ig kappa chain pre
11	410	72.8	101	2 S13701	Ig kappa chain V r
12	410	72.8	129	2 S52789	Ig kappa chain V r
13	399	70.9	75	2 A34966	Ig heavy chain V r
14	397	70.5	129	2 S36264	Ig lambda chain V
15	397	70.5	129	2 S40369	Ig kappa chain - h
16	397	70.5	132	2 S40334	Ig kappa chain - h
17	395	70.2	125	2 S40316	Ig kappa chain - h
18	394	70.0	108	1 K1HDM6	Ig kappa chain V-I
19	394	70.0	125	2 S40333	Ig kappa chain V-I
20	393	69.8	108	1 K1HDMU	Ig kappa chain V-I
21	393	69.8	108	1 I39154	Ig kappa chain V-I
22	393	69.8	108	2 B49047	Ig kappa chain (BR
23	392.5	69.7	106	2 C33936	Ig kappa chain V r
24	392	69.6	108	2 S19674	Ig kappa chain V r
25	391	69.4	108	1 K1HDMY	Ig kappa chain V-I
26	389	69.1	123	2 S40313	Ig kappa chain V-J
27	389	69.1	131	2 S40352	Ig kappa chain V-J
28	388.5	69.0	104	2 S26329	Ig kappa chain V r
29	388	68.9	108	1 K1HDMN	Ig kappa chain V-I

30	388	68.9	125	2 S09365	Ig kappa chain - m
31	386	68.6	107	2 B49026	Ig kappa chain V r
32	386	68.6	108	2 S19112	Ig kappa chain V r
33	386	68.6	125	2 S40349	Ig kappa chain V-J
34	385	68.4	108	2 S19970	Ig kappa chain V r
35	385	68.4	127	2 PH1224	Ig kappa chain pre
36	384	68.2	117	2 S46371	Ig kappa chain V-J
37	384	68.2	123	2 S40331	Ig kappa chain - h
38	384	68.2	129	2 S40317	Ig kappa chain - h
39	383.5	68.1	104	2 S26330	Ig kappa chain V r
40	383	68.0	108	1 K1HDM6	Ig kappa chain V-I
41	383	68.0	110	2 S44118	Ig kappa chain V-I
42	383	68.0	125	2 S40350	Ig kappa chain V-J
43	382.5	67.9	107	2 S16275	Ig kappa chain - h
44	382	67.9	108	1 K1HDMG	Ig kappa chain V-I
45	382	67.9	108	1 K1HDMU	Ig kappa chain V-I

ALIGNMENTS

```
RESULT 1
S52447
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52447
R:Berdoz, J.; Kraehenbuhl, J.P.
Submitted to the EMBL Data Library, November 1994
A:Description: Specific amplification by the polymerase chain reaction of rearranged ge
A:Reference number: S52445
A:Accession: S52447
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <BER>
A:Cross-references: EMBL:X82688; NID:g673443; PIDN:CAA58009.1; PID:g673444
C:Genetics:
A:Insertions: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match      97.0% Score 546; DB 2; Length 127;
Best Local Similarity 95.3%; Pred. No. 1.7e-39;
Matches 102; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIKWTQSPSSMYASLSGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      21 DIKVTQSPSSMYASLSGERVTITCKASQDINNYLWVFOQKPKSPKTLIYRANRLDGVPS 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61 RFGSGSGGQDYSLTISLSLEYEDMGITYCLOYDEPPTFGGTTKLEIK 107
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      81 RFGSGSGGQDYSLTISLSLEYEDMGITYCLOYDEPPTFGGTTKLEIK 127
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
KVMST1
Ig kappa chain precursor V region (T1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1980 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
C:Accession: A01920
R:Altendburger, W.; Steinmetz, M.; Zachau, H.G.
Nature 287, 603-607, 1980
A:Title: Functional and non-functional joining in immunoglobulin light chain genes of a
A:Reference number: A01920; MUID:81052342; PMID:6776411
A:Accession: A01920
A:Molecule type: mRNA
A:Residues: 1-128 <ALT>
A:Cross-references: UNIPROT:P01637; GB:V00772; NID:g51636; PIDN:CAA24150.1; PID:g762975
A>Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Insertions: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
```

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1g
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-128/Product: Ig kappa chain V region (T1) #status predicted <MAT>
 F:36-110/Domain: immunoglobulin homology <IMM>
 F:43-108/Disulfide bonds: #status predicted

Query Match 94.8%; Score 534; DB 1; Length 128;
 Best Local Similarity 93.5%; Pred. No. 1.7e-38;
 Matches 100; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKTLIYRANRLVDGVPS 60
 DB 21 DIKMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKTLIYRANRLVDGVPS 80
 QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYCLQYDEPPYTFGGGTLEIK 107
 DB 81 RFSGSGSGQDYSLTISLSEYEDMGIIYCYCLQYDEPPYTFGGGTLEIK 127

RESULT 3

Ig kappa chain precursor (15CS) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S14237
 R:Vandamme, A.M.; Bulens, F.; Bernart, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
 Eur. J. Biochem. 192, 767-775, 1990
 A>Title: Construction and characterization of a recombinant murine monoclonal antibody d
 A:Reference number: S14236; MUID:91006173; PMID:2209622
 A:Accession: S14237
 A:Molecule type: mRNA
 A:Residues: 1-234 <VNA>
 A:Cross-references: EMBL:X56394; NID:951622; PIDN:CAA39805.1; PID:951623
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 93.3%; Score 525; DB 2; Length 234;
 Best Local Similarity 91.6%; Pred. No. 1.8e-37;
 Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKTLIYRANRLVDGVPS 60
 DB 21 DIKMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKTLIYRANRLVDGVPS 80
 QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYCLQYDEPPYTFGGGTLEIK 107
 DB 81 RFSGSGSGQDYSLTISLSEYEDMGIIYCYCLQYDEPPYTFGGGTLEIK 127

RESULT 4

Ig kappa chain precursor V region (40-140) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
 C:Accession: P0101
 R:Neat, R.I.; Haber, E.
 Mol. Immunol. 26, 371-382, 1989
 A>Title: Characterization of the heavy and light chain immunoglobulin variable region ge
 A:Reference number: P01010; MUID:89238344; PMID:2497340
 A:Accession: P0101
 A:Molecule type: DNA
 A:Residues: 1-128 <NEA>
 A:Experimental source: strain A/J
 A>Note: the V40-140 gene segment can be classified as a member of the Vk9 subgroup
 C:Genetics:
 A:introns: 17/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-114/Domain: V segment #status predicted <VRA>

F:36-110/Domain: immunoglobulin homology <IMM>
 F:115-128/Domain: V segment #status predicted <VRA>

Query Match 92.2%; Score 519; DB 2; Length 128;
 Best Local Similarity 92.5%; Pred. No. 3.2e-37;
 Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKTLIYRANRLVDGVPS 60
 DB 21 DIKMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKTLIYRANRLVDGVPS 80
 QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYCLQYDEPPYTFGGGTLEIK 107
 DB 81 RFSGSGSGQDYSLTISLSEYEDMGIIYCYCLQYDEPPYTFGGGTLEIK 127

RESULT 5

Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S20652
 R:Gorman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
 Submitted to the EMBL Data Library, February 1992
 A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice reas
 A:Reference number: S20639
 A:Accession: S20652
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-106 <LOS>
 A:Cross-references: EMBL:X65008; NID:952649; PIDN:CAA46141.1; PID:952650
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.9%; Score 506; DB 2; Length 106;
 Best Local Similarity 89.6%; Pred. No. 3.4e-36;
 Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKTLIYRANRLVDGVPS 60
 DB 1 DIKMTQSPSSMYASISGERVITTCASQDINSYLSWFOQKPKSKTLIYRANRLVDGVPS 80
 QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYCLQYDEPPYTFGGGTLEIK 106
 DB 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYCLQYDEPPYTFGGGTLEIK 106

RESULT 6

Ig kappa chain precursor V region (L6) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
 C:Accession: A01921
 R:Rech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
 Nature 291, 668-670, 1981
 A>Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding seq
 A:Reference number: A93259; MUID:81220975; PMID:6264318
 A:Accession: A01921
 A:Molecule type: DNA
 A:Residues: 1-115 <PEC>
 A:Cross-references: UNIPROT:P01638; GB:V01563; GB:J00573; NID:951714; PIDN:CAA24893.1;
 A>Note: the sequence was determined from the germline gene
 C:Genetics:
 A:introns: 17/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kai
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1c
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-115/Product: Ig kappa chain V region (L6) #status predicted <MAT>
 F:36-110/Domain: immunoglobulin homology <IMM>
 F:43-108/Disulfide bonds: #status predicted

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 18:05:34 ; Search time 61.8643 Seconds
(without alignments)
622.182 Million cell updates/sec

Title: US-10-774-076-3

Perfect score: 563

Sequence: 1 DIKWTGSPSSMYASISGERVT.....CLQYDEPPTFGGCTLEIK 107

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	563	100.0	107	17	US-10-774-076-3
2	563	100.0	107	17	US-10-774-076-11
3	556	98.8	107	15	US-10-436-782-33
4	556	98.8	107	15	US-10-436-783-1
5	541	96.1	107	14	US-10-340-189-26
6	541	96.1	107	15	US-10-325-696-26
7	531	94.3	107	14	US-10-127-890-123
8	527	93.6	107	9	US-08-158-120A-21
9	522	92.7	142	9	US-08-797-481-2
10	522	92.7	142	9	US-09-844-736-4
11	522	92.7	142	14	US-10-162-396-4
12	522	92.7	142	17	US-10-819-493-4
13	508	90.2	107	14	US-10-340-189-27

14	508	90.2	107	15	US-10-325-696-27	Sequence 27, App1
15	503	89.3	107	17	US-10-774-076-14	Sequence 19, App1
16	503	89.3	107	17	US-10-774-076-19	Sequence 14, App1
17	487	86.5	107	14	US-10-127-890-125	Sequence 125, App
18	487	86.5	107	14	US-10-340-189-87	Sequence 87, App1
19	487	86.5	107	15	US-10-325-696-65	Sequence 65, App1
20	484	86.0	240	14	US-10-127-890-147	Sequence 147, App
21	484	86.0	240	14	US-10-127-890-148	Sequence 148, App
22	465	82.6	107	15	US-10-412-406-1	Sequence 1, App1
23	465	82.6	4852	15	US-10-412-406-33	Sequence 33, App1
24	464	82.4	107	15	US-10-462-062-148	Sequence 148, App
25	464	82.4	107	16	US-10-472-905A-100	Sequence 100, App
26	464	82.4	127	15	US-10-462-062-162	Sequence 162, App
27	464	82.4	127	16	US-10-472-905A-104	Sequence 104, App
28	463	82.2	129	15	US-10-462-062-147	Sequence 147, App
29	463	82.2	129	15	US-10-462-062-161	Sequence 161, App
30	458	81.3	107	9	US-09-158-120A-20	Sequence 20, App1
31	458	81.3	251	15	US-10-239-656-65	Sequence 65, App1
32	447	79.4	107	15	US-10-462-062-107	Sequence 107, App
33	447	79.4	107	16	US-10-472-905A-96	Sequence 96, App1
34	447	79.4	127	15	US-10-462-062-182	Sequence 182, App
35	447	79.4	127	16	US-10-472-905A-122	Sequence 122, App
36	443	78.7	109	10	US-09-802-083-3	Sequence 3, App1
37	443	78.7	109	14	US-10-165-732A-3	Sequence 3, App1
38	443	78.7	109	14	US-10-172-785-3	Sequence 3, App1
39	443	78.7	109	16	US-10-745-455-3	Sequence 3, App1
40	441	78.3	107	15	US-10-412-406-4	Sequence 4, App1
41	439	78.0	107	15	US-10-412-406-8	Sequence 8, App1
42	439	78.0	663	15	US-10-412-406-32	Sequence 32, App1
43	436	77.4	107	15	US-10-462-062-101	Sequence 101, App
44	436	77.4	107	16	US-10-472-905A-90	Sequence 90, App1
45	436	77.4	127	15	US-10-462-062-181	Sequence 181, App

ALIGNMENTS

RESULT 1
US-10-774-076-3
; Sequence 3, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Antiherpetic Antibodies and Their Use to Treat Cancer and
; TITLE OF INVENTION: Patentable
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10/774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 107
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-3

Query Match 100.0%; Score 563; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 66-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIKWTGSPSSMYASISGERVTITCKASODINSYTWQKRGKSPKTLIYRANLVGVPS 60
DB 1 DIKWTGSPSSMYASISGERVTITCKASODINSYTWQKRGKSPKTLIYRANLVGVPS 60
QY 61 RFGSGSGQDYSLTISLSEYEDMGIIYCCLOYDEPPTFGGCTLEIK 107
DB 61 RFGSGSGQDYSLTISLSEYEDMGIIYCCLOYDEPPTFGGCTLEIK 107
RESULT 2
US-10-774-076-11
; Sequence 11, Application US/10774076

Publication No. US20040210040A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Landolfi, et al.
TITLE OF INVENTION: Antihergulin Antibodies and Their Use to Treat Cancer and
FILE REFERENCE: 05882.0064.NPUS01
CURRENT APPLICATION NUMBER: US/10/774,076
CURRENT FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
LENGTH: 127
TYPE: PRT
ORGANISM: mus sp.
US-10-774-076-11

Query Match 100.0%; Score 563; DB 17; Length 127;
Best Local Similarity 100.0%; Pred. No. 7.2e-42;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 21 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 80
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYFGGTGLEIK 107
DB 81 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYFGGTGLEIK 127

RESULT 3

US-10-436-782-33
Sequence 33, Application US/10436782
Publication No. US20040028685A1
GENERAL INFORMATION:
APPLICANT: Kinch, Michael
APPLICANT: Carles-Kinch, Kelly
APPLICANT: Kiener, Peter
APPLICANT: Langemann, Solomon
TITLE OF INVENTION: EphA2 Monoclonal Antibodies and Methods of Use Thereof
FILE REFERENCE: 10271-097
CURRENT APPLICATION NUMBER: US/10/436,782
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,322
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2002-10-14
PRIOR APPLICATION NUMBER: 60/418,213
PRIOR FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
LENGTH: 107
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-436-782-33

Query Match 98.8%; Score 556; DB 15; Length 107;
Best Local Similarity 98.1%; Pred. No. 2.5e-41;
Matches 105; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYFGGTGLEIK 107
DB 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYFGGTGLEIK 107

RESULT 4
US-10-436-783-1
Sequence 1, Application US/10436783

Publication No. US20040091486A1
GENERAL INFORMATION:
APPLICANT: Kinch, Michael
APPLICANT: Carles-Kinch, Kelly
TITLE OF INVENTION: EphA2 Agonistic Monoclonal Antibodies and Methods of Use Thereof
FILE REFERENCE: 10271-107
CURRENT APPLICATION NUMBER: US/10/436,783
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: 60/379,368
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/418,204
PRIOR FILING DATE: 2002-10-14
PRIOR APPLICATION NUMBER: 60/460,358
PRIOR FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 107
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-436-783-1

Query Match 98.8%; Score 556; DB 15; Length 107;
Best Local Similarity 98.1%; Pred. No. 2.5e-41;
Matches 105; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 1 DIKMTQSPSSMYASISGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYFGGTGLEIK 107
DB 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCLQYDEFPYFGGTGLEIK 107

RESULT 5

US-10-340-189-26
Sequence 26, Application US/10340189
Publication No. US20030229207A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 W. Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TRIEUX: <Unknown>
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-340-189-26

Query Match 96.1%; Score 541; DB 14; Length 107;
Best Local Similarity 96.3%; Pred. No. 5,1e-40;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIRMTPSSSMVYASLGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 1 DIRMTPSSSMVYASLGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
QY 61 RFGSGSGGDYSLTISLSLEYEDMGITYCLOYDEFPYTFGGGTLEIK 107
DB 61 RFGSGSGGDYSLTISLSLEYEDMGITYCLOYDEFPYTFGGGTLEIK 107

RESULT 6

US-10-325-696-26
Sequence 26, Application US/10325696
Publication No. US20040005630A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9050
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-325-696-26

Query Match 96.1%; Score 541; DB 15; Length 107;
Best Local Similarity 96.3%; Pred. No. 5,1e-40;
Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIRMTPSSSMVYASLGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 1 DIRMTPSSSMVYASLGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
QY 61 RFGSGSGGDYSLTISLSLEYEDMGITYCLOYDEFPYTFGGGTLEIK 107
DB 61 RFGSGSGGDYSLTISLSLEYEDMGITYCLOYDEFPYTFGGGTLEIK 107

RESULT 7

US-10-127-890-123
Sequence 123, Application US/10127890
Publication No. US2003016196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-10-127-890-123
Query Match 94.3%; Score 531; DB 14; Length 107;

Best Local Similarity 94.4%; Pred. No. 3.9e-39;
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIRMTPSSSMYASLGERVTITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 1 DIRMTPSSSMYASLGERVTITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
QY 61 RFGSGSGGQDYSLTISLEYEDMGIIYCCQYDEFPYTFGGTGKLEIK 107
DB 61 RFGSGSGGQDYSLTISLEYEDMGIIYCCQYDEFPYTFGGTGKLEIK 107

RESULT 8

US-09-158-120A-21
Sequence 21, Application US/09158120A
Patent No. US20020102257A1
GENERAL INFORMATION:
APPLICANT: JOHNSON, L.
TITLE OF INVENTION: Human Murine Chimeric Antibodies Against
TITLE OF INVENTION: Respiratory Syncytial Virus
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: P160
OPERATING SYSTEM: Windows95
SOFTWARE: MS Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158, 120A
FILING DATE: September 21, 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,592
FILING DATE: August 15, 1994
APPLICATION NUMBER: 07/813,372
FILING DATE: December 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 469201-367
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-11744
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-158-120A-21

Query Match 93.6%; Score 527; DB 9; Length 107;
Best Local Similarity 92.5%; Pred. No. 8.7e-39;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIRMTPSSSMYASLGERVTITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 1 DIRMTPSSSMYASLGERVTITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
QY 61 RFGSGSGGQDYSLTISLEYEDMGIIYCCQYDEFPYTFGGTGKLEIK 107
DB 61 RFGSGSGGQDYSLTISLEYEDMGIIYCCQYDEFPYTFGGTGKLEIK 107

RESULT 9

US-09-797-481-2

Sequence 2, Application US/09797481
Patent No. US20010047083A1
GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya
Kohler, Heinz
Foon, Kenneth A.
TITLE OF INVENTION: MURINE ANTI-IDIOYPE ANTIBODY 3H1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/797,481
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/361,772
FILING DATE: 27-JUL-1999
APPLICATION NUMBER: US 08/579,940
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/365,484
FILING DATE: 28-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-797-481-2

Query Match 92.7%; Score 522; DB 9; Length 142;
Best Local Similarity 91.6%; Pred. No. 3.2e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIRMTPSSSMYASLGERVTITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 21 DIRMTPSSSMYASLGERVTITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDGVP 80
QY 61 RFGSGSGGQDYSLTISLEYEDMGIIYCCQYDEFPYTFGGTGKLEIK 107
DB 81 RFGSGSGGQDYSLTISLEYEDMGIIYCCQYDEFPYTFGGTGKLEIK 127

RESULT 10

US-09-844-736-4
Sequence 4, Application US/09844736
Patent No. US20020041872A1
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
CEA-ASSOCIATED TUMORS USING ANTI-IDIOYPE ANTIBODY 3H1
NUMBER OF SEQUENCES: 6

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 PAGE MILL ROAD
;; CITY: PALO ALTO
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/844,736
;; FILING DATE: 09-Apr-1997
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/838,692
;; FILING DATE: April 9, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Polizzi, Catherine M.
;; REGISTRATION NUMBER: 40,130
;; REFERENCE/DOCKET NUMBER: 30414-20004.01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 813-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 142 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-844-736-4
Query Match 92.7%; Score 522; DB 9; Length 142;
Best Local Similarity 91.6%; Pred. No. 3.2e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIRMTPSSSMYASLGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 21 DIRMTPSSSMYASLGERVTITCKASQDINGYLNWFOQEPKSPKTLIYRANRLIDGVP 80
QY 61 RFGSGSGGDYSLTISLSEYEDMGTYCLOYDEPPTFGGCTKLEIK 107
DB 81 RFGSGSGGDYSLTISLSEYEDMGTYCLOYDEPPTFGGCTKLEIK 127
RESULT 11
US-10-162-396-4
;; Sequence 4, Application US/10162396
;; Publication No. US20030077274A1
;; GENERAL INFORMATION:
;; APPLICANT: Chatterjee, Malaya
;; Poon, Kenneth A.
;; Chatterjee, Sunil K.
;; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
;; CEA-ASSOCIATED TUMORS USING ANTI-IDIOYPE ANTIBODY 3H1
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 PAGE MILL ROAD
;; CITY: PALO ALTO
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US 09/844,736

;; APPLICATION NUMBER: US/10/162,396
;; FILING DATE: 31-Jul-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/844,736
;; FILING DATE: April 27, 2001
;; APPLICATION NUMBER: US 08/838,692
;; FILING DATE: April 9, 1997
;; APPLICATION NUMBER: US 60/044,455
;; FILING DATE: April 12, 1996
;; APPLICATION NUMBER: US 08/631,085
;; FILING DATE: April 12, 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Polizzi, Catherine M.
;; REGISTRATION NUMBER: 40,130
;; REFERENCE/DOCKET NUMBER: 304142000402
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 813-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 142 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-162-396-4
Query Match 92.7%; Score 522; DB 14; Length 142;
Best Local Similarity 91.6%; Pred. No. 3.2e-38;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIRMTPSSSMYASLGERVTITCKASQDINSYLSWFOQKPKSPKTLIYRANRLVDGVP 60
DB 21 DIRMTPSSSMYASLGERVTITCKASQDINGYLNWFOQEPKSPKTLIYRANRLIDGVP 80
QY 61 RFGSGSGGDYSLTISLSEYEDMGTYCLOYDEPPTFGGCTKLEIK 107
DB 81 RFGSGSGGDYSLTISLSEYEDMGTYCLOYDEPPTFGGCTKLEIK 127
RESULT 12
US-10-819-493-4
;; Sequence 4, Application US/10819493
;; Publication No. US20040253230A1
;; GENERAL INFORMATION:
;; APPLICANT: Chatterjee, Malaya
;; Poon, Kenneth A.
;; Chatterjee, Sunil K.
;; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
;; CEA-ASSOCIATED TUMORS USING ANTI-IDIOYPE ANTIBODY 3H1
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 PAGE MILL ROAD
;; CITY: PALO ALTO
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/819,493
;; FILING DATE: 06-Apr-2004
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 10/162,396
;; FILING DATE: June 3, 2002
;; APPLICATION NUMBER: US 09/844,736

FILED DATE: April 27, 2001
APPLICATION NUMBER: US 08/838,692
FILING DATE: April 9, 1997
APPLICATION NUMBER: US 60/044,455
FILING DATE: April 12, 1996
APPLICATION NUMBER: US 08/631,085
FILING DATE: April 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jacobson, Jill
REGISTRATION NUMBER: 40,030
REFERENCE/DOCKET NUMBER: 30414200403
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-819-493-4

Query Match
Best Local Similarity 92.7%; Score 522; DB 17; Length 142;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIRMTPSSMYASLGERVITTCASODINSYLSWFOQKPKGKPKTLIYRANRLVDGVPS 60
DB 21 DIRMTPSSMYASLGERVITTCASODINSYLSWFOQKPKGKPKTLIYRANRLVDGVPS 80

QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYLQYDEFPYTFGGTKLEIK 107
DB 81 RFSGSGSGQDYSLTISLSEYEDMGIIYCYLQYDEFPYTFGGTKLEIK 127

RESULT 13
US-10-340-189-27
Sequence 27, Application US/10340189
Publication No. US20030229207A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESSES: McAndrews, Held & Malloy, Ltd.
STREET: 500 W. Madison Street, 34th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-340-189-27

Query Match
Best Local Similarity 90.2%; Score 508; DB 14; Length 107;
Matches 96; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIRMTPSSMYASLGERVITTCASODINSYLSWFOQKPKGKPKTLIYRANRLVDGVPS 60
DB 1 DIRMTPSSMYASLGERVITTCASODINSYLSWFOQKPKGKPKTLIYRANRLVDGVPS 60

QY 61 RFSGSGSGQDYSLTISLSEYEDMGIIYCYLQYDEFPYTFGGTKLEIK 107
DB 61 RFSGSGSGTDYTLTISLSEYEDMGIIYCYLQYDESPWTFGGTKLEIK 107

RESULT 14
US-10-325-696-27
Sequence 27, Application US/10325696
Publication No. US20040005630A1
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESSES:
ADDRESSES: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,696
FILING DATE: 18-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/097,980
FILING DATE: 16-JUN-1998
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Janet M. McNicholas, Ph.D.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9050
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 27;
US-10-325-696-27

Query Match 90.2%; Score 508; DB 15; Length 107;
Best Local Similarity 89.7%; Pred. No. 4e-37;
Matches 96; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDSVPS 60
DB 1 DIKMTQSPSSMSASLSDRVITITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDSVPS 60

QY 61 RFSGSGSGGDYSLTISLSEYEDMGIIYYCLQYDEFPYTFGGGTLEIK 107
DB 61 RFSGSGSGDYLTLTISLSEYEDFGIYCCQYDESPWTFGGGTLEIK 107

RESULT 15
US-10-774-076-14

; Sequence 14, Application US/10774076
; Publication No. US20040210040A1

; GENERAL INFORMATION:

; APPLICANT: Protein Design Labs, Inc.

; APPLICANT: Landolfi, et al.

; TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and

; FILE REFERENCE: 05882.0064.NPUS01

; CURRENT APPLICATION NUMBER: US/10/774,076

; CURRENT FILING DATE: 2004-02-06

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 14

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Humanized antibody

US-10-774-076-14

Query Match 89.3%; Score 503; DB 17; Length 107;
Best Local Similarity 87.9%; Pred. No. 1.1e-36;
Matches 94; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIKMTQSPSSMYASISGERVTITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDSVPS 60
DB 1 DIKMTQSPSSLSASVGDRTITITCKASODINSYLSWFOQKPKSPKTLIYRANRLVDSVPS 60

QY 61 RFSGSGSGGDYSLTISLSEYEDMGIIYYCLQYDEFPYTFGGGTLEIK 107
DB 61 RFSGSGSGDYLTLTISLSEYEDFPATYYCQYDEFPYTFGGGTVEIK 107

Search completed: December 29, 2004, 18:41:57
Job time: 64.8643 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 29, 2004, 18:05:34 ; Search time 68.8024 Seconds
(without alignments)
622.182 Million cell updates/sec

Title: US-10-774-076-2

Perfect score: 648
Sequence: 1 EIDLOQSGPELVKPGASVKV.....GNFPYFDYWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppa/US10D_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	648	100.0	119	US-10-774-076-2	Sequence 2, App11
2	648	100.0	138	US-10-774-076-9	Sequence 9, App11
3	564	87.0	119	US-10-774-076-12	Sequence 12, App11
4	564	87.0	138	US-10-774-076-17	Sequence 17, App11
5	560.5	86.5	118	US-10-462-062-139	Sequence 139, App
6	560.5	86.5	118	US-10-462-062-140	Sequence 140, App
7	560.5	86.5	137	US-10-462-062-153	Sequence 153, App
8	560.5	86.5	137	US-10-462-062-154	Sequence 154, App
9	548.5	84.6	120	US-10-372-719-2	Sequence 2, App11
10	529	81.6	117	US-10-223-880-2	Sequence 2, App11
11	523.5	80.8	139	US-10-365-123-28	Sequence 28, App11
12	517	79.8	117	US-10-383-447-14	Sequence 14, App11
13	517	79.8	117	US-10-769-612-3	Sequence 3, App11

14	514.5	79.4	152	US-10-642-120-2	Sequence 2, App11
15	514.5	79.4	152	US-10-642-060-2	Sequence 2, App11
16	514.5	79.4	152	US-10-642-123-2	Sequence 2, App11
17	514.5	79.4	152	US-10-642-124-2	Sequence 2, App11
18	514.5	79.4	152	US-10-621-269-2	Sequence 2, App11
19	514.5	79.4	152	US-10-620-850-2	Sequence 2, App11
20	514.5	79.4	152	US-10-642-118-2	Sequence 2, App11
21	514.5	79.4	152	US-10-642-119-2	Sequence 2, App11
22	514.5	79.4	152	US-10-642-099-2	Sequence 2, App11
23	514.5	79.4	152	US-10-642-099-2	Sequence 2, App11
24	512.5	79.1	118	US-10-462-062-144	Sequence 144, App
25	512.5	79.1	137	US-10-462-062-158	Sequence 158, App
26	503.5	77.7	10	US-09-940-727B-90	Sequence 90, App1
27	503.5	77.7	118	US-10-462-062-143	Sequence 143, App
28	503.5	77.7	15	US-10-462-062-157	Sequence 157, App
29	502	77.5	137	US-09-215-163-44	Sequence 44, App1
30	498.5	76.9	116	US-09-940-727B-14	Sequence 14, App1
31	496	76.5	10	US-09-990-586-4	Sequence 4, App11
32	496	76.5	117	US-10-310-113-4	Sequence 4, App11
33	496	76.5	117	US-10-230-880-4	Sequence 4, App11
34	494	76.2	136	US-10-768-193-7	Sequence 7, App11
35	492	75.9	117	US-09-293-854-4	Sequence 4, App11
36	492	75.9	117	US-10-293-417-4	Sequence 4, App11
37	492	75.9	117	US-10-764-140-4	Sequence 4, App11
38	490.5	75.7	116	US-10-389-155-15	Sequence 15, App1
39	490.5	75.7	116	US-10-389-417-15	Sequence 15, App1
40	490.5	75.7	116	US-10-452-357-56	Sequence 56, App1
41	490.5	75.7	135	US-10-389-155-60	Sequence 60, App1
42	490.5	75.7	135	US-10-389-417-60	Sequence 60, App1
43	490.5	75.7	135	US-10-452-357-69	Sequence 69, App1
44	490	75.6	117	US-10-816-938-10	Sequence 10, App1
45	490	75.6	130	US-09-839-447A-3	Sequence 3, App11

ALIGNMENTS

RESULT 1
US-10-774-076-2
; Sequence 2, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Antiherpetic Antibodies and Their Use to Treat Cancer and
; FILE REFERENCE: 05882.0064.NPUS01
; CURRENT APPLICATION NUMBER: US/10774,076
; CURRENT FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-2

Query Match 100.0%; Score 648; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.7e-52;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIDLOQSGPELVKPGASVKVSCASGYPFNNMVKSHGKSLKIGTIDYDGPY 60
DB 1 EIDLOQSGPELVKPGASVKVSCASGYPFNNMVKSHGKSLKIGTIDYDGPY 60

QY 61 SOKPKGATLVTKSSSTAYMHLNSLTSESAVYYCARRGNPFYFDYWGQGTTLTVSS 119
DB 61 SOKPKGATLVTKSSSTAYMHLNSLTSESAVYYCARRGNPFYFDYWGQGTTLTVSS 119

RESULT 2
US-10-774-076-9
; Sequence 9, Application US/10774076

Publication No. US20040210040A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Landolfi, et al.
TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
TITLE OF INVENTION: Psoriasis
FILE REFERENCE: 05882.0064.NPUS01
CURRENT APPLICATION NUMBER: US/10/774,076
CURRENT FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
LENGTH: 138
TYPE: PRT
ORGANISM: mus sp.
US-10-774-076-9

Query Match 100.0%; Score 648; DB 17; Length 138;
Best Local Similarity 100.0%; Pred. No. 3.1e-52;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIQLQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLFWIGYIDPYGDPGY 60
DB 20 EVQLVDSGAEVKKPKASVKISCKVSGYAFNTNMYWVKSHGKSLFWIGYIDPYGDPGY 79
QY 61 SQKFKGKATLTVDKSSSTAYMHLNLSLTSBDSAVYYCARNGFPYFDYWGQGTTLTVSS 119
DB 80 SQKFKGKATLTVDKSSSTAYMHLNLSLTSBDSAVYYCARNGFPYFDYWGQGTTLTVSS 138

RESULT 3

US-10-774-076-12
Sequence 12, Application US/10774076
Publication No. US20040210040A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Landolfi, et al.
TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
TITLE OF INVENTION: Psoriasis
FILE REFERENCE: 05882.0064.NPUS01
CURRENT APPLICATION NUMBER: US/10/774,076
CURRENT FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Humanized antibody
US-10-774-076-12

Query Match 87.0%; Score 564; DB 17; Length 119;
Best Local Similarity 84.9%; Pred. No. 1.6e-44;
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIQLQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLFWIGYIDPYGDPGY 60
DB 1 EVQLVDSGAEVKKPKASVKISCKVSGYAFNTNMYWVKSHGKSLFWIGYIDPYGDPGY 60
QY 61 SQKFKGKATLTVDKSSSTAYMHLNLSLTSBDSAVYYCARNGFPYFDYWGQGTTLTVSS 119
DB 61 SQKFKGKATLTVDKSSSTAYMHLNLSLTSBDSAVYYCARNGFPYFDYWGQGTTLTVSS 119

RESULT 4

US-10-774-076-17
Sequence 17, Application US/10774076
Publication No. US20040210040A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Landolfi, et al.
TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and

TITLE OF INVENTION: Psoriasis
FILE REFERENCE: 05882.0064.NPUS01
CURRENT APPLICATION NUMBER: US/10/774,076
CURRENT FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 138
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Humanized antibody
US-10-774-076-17

Query Match 87.0%; Score 564; DB 17; Length 138;
Best Local Similarity 84.9%; Pred. No. 1.8e-44;
Matches 101; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 EIQLQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLFWIGYIDPYGDPGY 60
DB 20 EVQLVDSGAEVKKPKASVKISCKVSGYAFNTNMYWVKSHGKSLFWIGYIDPYGDPGY 79
QY 61 SQKFKGKATLTVDKSSSTAYMHLNLSLTSBDSAVYYCARNGFPYFDYWGQGTTLTVSS 119
DB 80 SQKFKGKATLTVDKSSSTAYMHLNLSLTSBDSAVYYCARNGFPYFDYWGQGTTLTVSS 138

RESULT 5

US-10-462-062-139
Sequence 139, Application US/10462062
Publication No. US20040044187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 139
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of
US-10-462-062-139

Query Match 86.5%; Score 560.5; DB 15; Length 118;
Best Local Similarity 89.9%; Pred. No. 3.3e-44;
Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQLQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLFWIGYIDPYGDPGY 60
DB 1 EIQLQSGPELVKPGASVYKSCASGYAFNTNMYWVKSHGKSLFWIGYIDPYGDPGY 60
QY 61 SQKFKGKATLTVDKSSSTAYMHLNLSLTSBDSAVYYCARNGFPYFDYWGQGTTLTVSS 119
DB 61 SQKFKGKATLTVDKSSSTAYMHLNLSLTSBDSAVYYCARNGFPYFDYWGQGTTLTVSS 118

RESULT 6

US-10-462-062-140
Sequence 140, Application US/10462062
Publication No. US20040044187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH

APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ. ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 140
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of
OTHER INFORMATION: H chain V region of anti TF mouse monoclonal antibody ATR-3
US-10-462-062-140

Query Match 86.5%; Score 560.5; DB 15; Length 118;
Best Local Similarity 89.9%; Pred. No. 3.3e-44;
Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQLOOQSGPELVKPGASVSKVSCASGVAFTNNMWWYWKOSHGKSLWIGYIDPYGDPGY 60
DB 1 EIQLOOQSGPELVKPGASVSKVSCASGVSFTDYNMWWYWKOSHGKSLWIGYIDPYNGGTIY 60
61 SOKFKGKATLTVDKSSSTAVMHLNLSLTSBDSAVYYCARRGNFPYYPDWGQGTTLTVSS 119
DB 61 NOKFKGKATLTVDKSSSTAFMHLNLSLTSBDSAVYYCARGGE-GYFPYWGQGTTLTVSS 118

RESULT 7
US-10-462-062-153
Sequence 153, Application US/10462062
Publication No. US2004004187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ. ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 153
LENGTH: 137
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal
US-10-462-062-153

Query Match 86.5%; Score 560.5; DB 15; Length 137;
Best Local Similarity 89.9%; Pred. No. 3.9e-44;
Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQLOOQSGPELVKPGASVSKVSCASGVAFTNNMWWYWKOSHGKSLWIGYIDPYGDPGY 60
DB 20 EIQLOOQSGPELVKPGASVSKVSCASGVSFTDYNMWWYWKOSHGKSLWIGYIDPYNGGTIY 79
QY 61 SOKFKGKATLTVDKSSSTAVMHLNLSLTSBDSAVYYCARRGNFPYYPDWGQGTTLTVSS 119
DB 80 NOKFKGKATLTVDKSSSTAFMHLNLSLTSBDSAVYYCARGGE-GYFPYWGQGTTLTVSS 137

RESULT 8
US-10-462-062-154
Sequence 154, Application US/10462062
Publication No. US2004004187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ. ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 154
LENGTH: 137
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal
US-10-462-062-154

Query Match 86.5%; Score 560.5; DB 15; Length 137;
Best Local Similarity 89.9%; Pred. No. 3.9e-44;
Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQLOOQSGPELVKPGASVSKVSCASGVAFTNNMWWYWKOSHGKSLWIGYIDPYGDPGY 60
DB 20 EIQLOOQSGPELVKPGASVSKVSCASGVSFTDYNMWWYWKOSHGKSLWIGYIDPYNGGTIY 79
QY 61 SOKFKGKATLTVDKSSSTAVMHLNLSLTSBDSAVYYCARRGNFPYYPDWGQGTTLTVSS 119
DB 80 NOKFKGKATLTVDKSSSTAFMHLNLSLTSBDSAVYYCARGGE-GYFPYWGQGTTLTVSS 137

RESULT 9
US-10-372-719-2
Sequence 2, Application US/10372719
Publication No. US20040005643A1
GENERAL INFORMATION:
APPLICANT: DE SANTIS, RITA
APPLICANT: ANASTASI, ANNA MARIA
TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY
FILE REFERENCE: 2818-141
CURRENT APPLICATION NUMBER: US/10/372,719
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 60/359,299
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ. ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: ST2146 heavy chain variable region protein sequence
US-10-372-719-2

Query Match 84.5%; Score 548.5; DB 15; Length 120;
Best Local Similarity 86.7%; Pred. No. 4.3e-43;
Matches 104; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIQLOOQSGPELVKPGASVSKVSCASGVAFTNNMWWYWKOSHGKSLWIGYIDPYGDPGY 60
DB 1 EIQLOOQSGPELVKPGASVSKVSCASGVAFTNNMWWYWKOSHGKSLWIGYIDPYNGGTIY 79

Db 1 KYLQOQSGPELVKPGASVYKSCASGYAFTSYNMVWKSHGKSLWIGYIDPNKGVTSY 60
 QY 61 SQRKKGATLTVDKSSSTAYMHLNLSLTSEDSAVYYCARGNFPYY-FDYWGQGTTLTVSS 119
 Db 61 NQFKKGATLTVDKSSSTAYMHLNLSLTSEDSAVYYCARGGSIYYAMDYWGQGTTLTVSS 120

RESULT 10
 US-10-223-880-2
 ; Sequence 2, Application US/10223880
 ; Publication No. US20030152571A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JONAK, ZDENKA
 ; APPLICANT: JOHANSON, KYUNG O.
 ; APPLICANT: TAYLOR, ALEXANDER
 ; TITLE OF INVENTION: ANTI-ALPHA-BETA3 HUMANIZED MONOCLONAL
 ; TITLE OF INVENTION: ANTIBODIES
 ; FILE REFERENCE: P50629C1
 ; CURRENT APPLICATION NUMBER: US/10/223,880
 ; CURRENT FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: 09/380,910
 ; PRIOR FILING DATE: 1999-09-10
 ; PRIOR APPLICATION NUMBER: PCT/US98/04987
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/039,609
 ; PRIOR FILING DATE: 1997-03-12
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 117
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-223-880-2

Query Match 81.6%; Score 529; DB 14; Length 117;
 Best Local Similarity 84.3%; Pred. No. 2,7e-41;
 Matches 102; Conservative 8; Mismatches 5; Indels 6; Gaps 2;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFTSYNMVWKSHGKSLWIGYIDPNKGVTSY 60
 Db 1 EIQLOQSGPELVKPGASVYKSCASGYAFTSYNMVWKSHGKSLWIGYIDPNKGVTSY 60
 QY 61 SQRKKGATLTVDKSSSTAYMHLNLSLTSEDSAVYYCAR--GNPYYFDYWGQGTTLTVSS 118
 Db 61 NQFKKGATLTVDKSSSTAYMHLNLSLTSEDSAVYYCARQYGSFA---YWGQGTTLTVSS 116
 QY 119 S 119
 Db 117 A 117

RESULT 11
 US-10-365-123-28
 ; Sequence 28, Application US/10365123
 ; Publication No. US20040053365A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Renner, Christoph
 ; APPLICANT: Scott, Andrew
 ; APPLICANT: Burgess, Antony
 ; TITLE OF INVENTION: HUMANIZED GM-CSF ANTIBODIES
 ; FILE REFERENCE: LUD 5729.1
 ; CURRENT APPLICATION NUMBER: US/10/365,123
 ; CURRENT FILING DATE: 2003-02-12
 ; NUMBER OF SEQ ID NOS: 56
 ; SEQ ID NO 28
 ; LENGTH: 139
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region
 US-10-365-123-28

Query Match 80.8%; Score 523.5; DB 15; Length 139;

Best Local Similarity 81.5%; Pred. No. 1e-40;
 Matches 97; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFTSYNMVWKSHGKSLWIGYIDPNKGVTSY 60
 Db 18 EVDLQOQSGPELVKPGASVYKSCASGYAFTSYNMVWKSHGKSLWIGYIDPNKGVTSY 77
 QY 61 SQRKKGATLTVDKSSSTAYMHLNLSLTSEDSAVYYCARGNFPYYFDYWGQGTTLTVSS 119
 Db 78 NQFKKGATLTVDKSSSTAYMHLNLSLTSEDSAVYYCARDRFP-YFDYWGQGTTLTVSS 135

RESULT 12
 US-10-383-447-14
 ; Sequence 14, Application US/10383447
 ; Publication No. US20040096392A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bhaskar, Vinay
 ; APPLICANT: de la Calle, Agustin
 ; APPLICANT: Law, Debbie
 ; APPLICANT: Carae, Ingrid
 ; APPLICANT: Ramakrishnan, Vanitha
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Afar, Daniel
 ; APPLICANT: Powers, David
 ; TITLE OF INVENTION: Antibodies Against Cancer Antigen TWEFP2 and Uses Thereof
 ; FILE REFERENCE: 05882.0133.NPUS00
 ; CURRENT APPLICATION NUMBER: US/10/383,447
 ; CURRENT FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: US 60/362,837
 ; PRIOR FILING DATE: 2002-03-08
 ; PRIOR APPLICATION NUMBER: US 60/463,812
 ; PRIOR FILING DATE: 2002-12-27
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 14
 ; LENGTH: 117
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Heavy chain variable region
 US-10-383-447-14

Query Match 79.8%; Score 517; DB 15; Length 117;
 Best Local Similarity 82.4%; Pred. No. 3.4e-40;
 Matches 98; Conservative 9; Mismatches 10; Indels 2; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFTSYNMVWKSHGKSLWIGYIDPNKGVTSY 60
 Db 1 EIQLOQSGPELVKPGASVYKSCASGYAFTSYNMVWKSHGKSLWIGYIDPNKGVTSY 60
 QY 61 SQRKKGATLTVDKSSSTAYMHLNLSLTSEDSAVYYCARGNFPYYFDYWGQGTTLTVSS 119
 Db 61 NQFKKGATLTVDKSSSTAYMHLNLSLTSEDSAVYYCVTYGS--DYFDYWGQGTTLTVSS 117

RESULT 13
 US-10-769-612-3
 ; Sequence 3, Application US/10769612
 ; Publication No. US20040141983A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Law, Debbie
 ; APPLICANT: Giesh, Kurt C.
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Culp, Patricia
 ; TITLE OF INVENTION: Compositions Against Cancer Antigen LIV-1 And Uses Thereof
 ; FILE REFERENCE: 05882.0129.CPUS08
 ; CURRENT APPLICATION NUMBER: US/10/769,612
 ; CURRENT FILING DATE: 2004-01-29
 ; PRIOR APPLICATION NUMBER: 60/443,712
 ; PRIOR FILING DATE: 2003-01-29
 ; PRIOR APPLICATION NUMBER: 09/642,034
 ; PRIOR FILING DATE: 2000-08-18


```
; PRIOR APPLICATION NUMBER: 09/525,361
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 09/453,137
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 09/450,810
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/268,865
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 117
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-769-612-3
```

```
Query Match      79.4%; Score 517; DB 16; Length 117;
Best Local Similarity 82.4%; Pred. No. 3,4e-40;
Matches 96; Conservative 9; Mismatches 10; Indels 2; Gaps 1;
```

```
QY 1 EIQLOQSGPELVKPGASVKVSCKASGYAFITNNMYYWKQSHGKSLIEWIGYIDPYGDPGY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EIQLOQSGPELVKPGASVKVSCKASGYAFITNNMYYWKQSHGKSLIEWIGYIDPYGDPGY 60
QY 61 SQFKGKATLTVDKSSSTAYMHLNLSITSEDSAVYYCARRGNF-PYFPDYGQGTTLTVSS 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 NQFKRGATLTVDKSSSTAYMHLNLSITSEDSAVYYCVTVSS--DYFPDYGQGTTLTVSS 117
```

RESULT 14

```
US-10-642-120-2
; Sequence 2, Application US/10642120
; Publication No. US20040131610A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia
; TITLE OF INVENTION: Methods for Treating Viral Infections Using Antibodies to
; FILE REFERENCE: 4001.002900
; CURRENT APPLICATION NUMBER: US/10/642,120
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 152
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-642-120-2
```

```
Query Match      79.4%; Score 514.5; DB 16; Length 152;
Best Local Similarity 80.0%; Pred. No. 7,7e-40;
Matches 96; Conservative 10; Mismatches 13; Indels 1; Gaps 1;
```

```
QY 1 EIQLOQSGPELVKPGASVKVSCKASGYAFITNNMYYWKQSHGKSLIEWIGYIDPYGDPGY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 EIQLOQSGPELVKPGASVKVSCKASGYAFITNNMYYWKQSHGKSLIEWIGYIDPYGDPGY 79
QY 61 SQFKGKATLTVDKSSSTAYMHLNLSITSEDSAVYYCARRGNF-PYFPDYGQGTTLTVSS 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NQFKRGATLTVDKSSSTAYMHLNLSITSEDSAVYYCVKGGYGYHWFVDVAGATTVTVSS 139
```

RESULT 15

```
US-10-642-060-2
; Sequence 2, Application US/10642060
; Publication No. US20040131621A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
```

```
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia
; TITLE OF INVENTION: Combinations and Kits for Treating Viral Infections Using Antibo
; FILE REFERENCE: 4001.002982
; CURRENT APPLICATION NUMBER: US/10/642,060
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 152
; TYPE: PRF
; ORGANISM: Mus musculus
US-10-642-060-2
```

```
Query Match      79.4%; Score 514.5; DB 16; Length 152;
Best Local Similarity 80.0%; Pred. No. 7,7e-40;
Matches 96; Conservative 10; Mismatches 13; Indels 1; Gaps 1;
```

```
QY 1 EIQLOQSGPELVKPGASVKVSCKASGYAFITNNMYYWKQSHGKSLIEWIGYIDPYGDPGY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 20 EIQLOQSGPELVKPGASVKVSCKASGYAFITNNMYYWKQSHGKSLIEWIGYIDPYGDPGY 79
QY 61 SQFKGKATLTVDKSSSTAYMHLNLSITSEDSAVYYCARRGNF-PYFPDYGQGTTLTVSS 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 80 NQFKRGATLTVDKSSSTAYMHLNLSITSEDSAVYYCVKGGYGYHWFVDVAGATTVTVSS 139
```

Search completed: December 29, 2004, 18:41:54
Job time : 74.8024 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:37:57 ; Search time 81.7906 Seconds
(without alignments)
521.928 Million cell updates/sec

Title: US-10-774-076-2

Perfect score: 648
Sequence: I EIQLOQSGPLVKGASVKV.....GNPPYEDYWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560.5	86.5	118	2	AAV52755 Anti-F188
2	560.5	86.5	118	2	AAV52756 Anti-F188
3	548.5	84.6	120	7	ABR82930 Anti-huma
4	541	83.5	140	7	ADC24943 Mouse 19/
5	541	83.5	140	7	ADK51711 Murine 19
6	529.5	81.7	116	2	AAW95481 Mouse der
7	529	81.6	117	2	AAW84093 Murine vi
8	525.5	81.1	214	6	ABP96759 TSH recep
9	525.5	81.1	214	6	ABP96760 TSH recep
10	520.5	80.3	214	6	ABP96763 TSH recep
11	520.5	80.3	214	6	ABP96764 TSH recep
12	518.5	80.0	239	7	ADC79231 Anti-CA12
13	517	79.8	117	7	ADC27445 TM6FP210
14	516.5	79.7	214	6	ABP96756 TSH recep
15	516.5	79.7	214	6	ABP96755 TSH recep
16	514.5	79.4	152	8	ADJ57084 3G4 anti-b
17	514.5	79.4	159	8	ADJ57088 3G4-28VH-
18	512.5	79.1	118	2	AAV52760 Anti-F188
19	512	79.0	112	5	AAE15811 Human mab
20	507.5	78.3	239	7	ADC79232 Control s
21	506.5	78.2	135	2	AAE28669 p12-h2. 3
22	505	77.9	267	3	AAW71882 Anti-Fas
23	504.5	77.9	116	3	AAW71882 Anti-Fas
24	504.5	77.9	116	3	AAW71882 Anti-Fas
25	504.5	77.9	130	2	AAW71886 Anti-Fas

ALIGNMENTS

26	504.5	77.9	135	2	AAW60866 Variable
27	504.5	77.9	135	2	AAW60293 IGM chime
28	504.5	77.9	457	3	AAW8408 Mouse vit
29	504.5	77.9	590	2	AAW31751 H chain s
30	504.5	77.9	590	2	AAW71888 Anti-huma
31	504.5	77.9	590	3	AAW12908 Anti-huma
32	503.5	77.7	116	2	AAW39889 Heavy cha
33	503.5	77.7	118	2	AAV52759 Anti-F188
34	502.5	77.5	116	2	AAW60864 Variable
35	502	77.5	119	2	AAW21819 1B10 ant
36	501.5	77.4	120	8	AD126469 Murine 14
37	501.5	77.4	162	2	AAW01752 MH1 monoc
38	499.5	77.1	137	2	AAW05090 Heavy cha
39	498.5	76.9	116	2	AAW39810 Variable
40	497.5	76.8	263	2	AAW90226 Anti-B7.2
41	497.5	76.8	268	2	AAW90222 Anti-B7.2
42	497.5	76.8	580	2	AAW90217 Bispectif
43	496	76.5	117	2	AAW71288 Human ant
44	496	76.5	117	6	ABR42700 Anti-F188
45	496	76.5	117	6	ABR42718 Anti-F188

RESULT 1
AAV52755
ID AAV52755 standard; protein; 118 AA.
AC AAV52755;
XX
XX
DT 26-JUN-2000 (first entry)
XX
XX
DE Anti-tissue factor mouse monoclonal antibody ATR-2 H chain V region.
XX
XX Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KM ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; chromobiotic disease; DIC;
KW disseminated intravascular coagulation; immunogenicity; chimeric.
XX
XX Synthetic.
OS Mus sp.
XX
PN WO9951743-A1.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-JP001768.
XX
PR 03-APR-1998; 98UP-00091850.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
XX Sato K, Adachi H, Yabuta N;
PI WPI; 1999-620204/53.
XX
XX N-PSDB; AA233006.
DR Humanised antibody recognizing human tissue factor, used for treatment of
XX disseminated intravascular coagulation.
XX
PS Claim 1; Page 274; 291pp; Japanese.
XX
XX The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hrf) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC containing the variable region of the L chain of a mouse monoclonal Ab
CC recognising human tissue factor (hrf) and the constant region of the L
CC chain of a human Ab, the variable region being one of six specified
CC sequences (which are the L chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment

CC and prevention of thrombotic disease, especially of disseminated
 CC intravascular coagulation (DIC). The humanised antibody has the high htf
 CC binding activity of the mouse monoclonal antibody but greatly reduced
 CC immunogenicity. AA233001 to AA233091 and Y527007 to AA52767 represent
 CC sequences used in the exemplification of the present invention
 XX
 XX Sequence 118 AA;

Query Match 86.5%; Score 560.5; DB 2; Length 118;
 Best Local Similarity 89.9%; Pred. No. 5.7e-40;
 Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMMVWKSHGKSLMWIGYIDPYGDPGY 60
 DB 1 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMMVWKSHGKSLMWIGYIDPYGDPGY 60
 QY 61 SOKFKGKATLTVDKSSSTVMHNLSTSDSAVYTCARNGNPFYFDYGGGTTLVSS 119
 DB 61 NQKFKGKATLTVDKSSSTVMHNLSTSDSAVYTCARNGE-GYFDYWGQGTTLTVSS 118

RESULT 2

ID AA52756 standard; protein, 118 AA.
 AC AA52756;

DT 26-JAN-2000 (first entry)

DE Anti-tissue factor mouse monoclonal antibody ATR-3 H chain V region.

KM Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
 KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
 KW disseminated intravascular coagulation; immunogenicity; chimeric.

OS Synthetic.
 OS Mus sp.

PN W09951743-A1.

PD 14-OCT-1999.

PF 02-APR-1999; 99WO-JP001768.

PR 03-APR-1998; 98JP-00091850.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Sato K, Adachi H, Yabuta N;

PT WPI; 1999-620204/53.

DR N-PSDB; AA233007.

PT Humanised antibody recognizing human tissue factor, used for treatment of
 PT disseminated intravascular coagulation.

PS Claim 1; Page 275; 291pp; Japanese.

XX The present invention describes chimeric antibody (Ab) heavy (H) chains
 CC containing the variable region of the H chain of a mouse monoclonal Ab
 CC recognizing human tissue factor (htf) and the constant region of the H
 CC chain of a human Ab. The variable region is one of six specified
 CC sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
 CC containing the variable region of the L chain of a mouse monoclonal Ab
 CC recognizing human tissue factor (htf) and the constant region of the L
 CC chain of a human Ab, the variable region being one of six specified
 CC sequences (which are the L chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
 CC and prevention of thrombotic disease, especially of disseminated
 CC intravascular coagulation (DIC). The humanised antibody has the high htf
 CC binding activity of the mouse monoclonal antibody but greatly reduced
 CC immunogenicity. AA233001 to AA233091 and Y527007 to AA52767 represent

CC sequences used in the exemplification of the present invention
 XX
 XX Sequence 118 AA;

Query Match 86.5%; Score 560.5; DB 2; Length 118;
 Best Local Similarity 89.9%; Pred. No. 5.7e-40;
 Matches 107; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMMVWKSHGKSLMWIGYIDPYGDPGY 60
 DB 1 EIQLOQSGPELVKPGASVYKSCASGYAFNTNMMVWKSHGKSLMWIGYIDPYGDPGY 60
 QY 61 SOKFKGKATLTVDKSSSTVMHNLSTSDSAVYTCARNGNPFYFDYGGGTTLVSS 119
 DB 61 NQKFKGKATLTVDKSSSTVMHNLSTSDSAVYTCARNGE-GYFDYWGQGTTLTVSS 118

RESULT 3

ID ABR82930 standard; protein, 120 AA.
 AC ABR82930;

DT 18-DEC-2003 (first entry)

DE Anti-human tenascin ST2146 Mab heavy chain variable region (VH).

KM ST2146; tenascin C; monoclonal antibody; EGF; epidermal growth factor;
 KW cytostatic; antibody therapy; vaccine.

OS Synthetic.

PN W02003072608-A1.

PD 04-SEP-2003.

PF 20-FEB-2003; 2003WO-IT000098.

PR 26-FEB-2002; 2002US-0359299P.

PA (SIGT) SIGMA-TAU IND FARM RIUNITE SPA.

PI De Santis R, Anastasi AM;

PT WPI; 2003-679945/64.

DR N-PSDB; ACR36519; ACR36531.

PT New anti-human tenascin ST2146 monoclonal antibody, and its proteolytic
 PT fragments that bind to an antigenic epitope within the EGF-like repeat of
 PT human tenascin C, useful for treating tumors, e. g. gliomas, cystic brain
 PT tumors.

PS Claim 1; Fig 11; 55pp; English.

XX The invention relates to an anti-human tenascin ST2146 monoclonal
 CC antibody (Mab) whose light and heavy chain variable region sequences and
 CC their proteolytic fragments that bind to an antigenic epitope within the
 CC EGF (epidermal growth factor)-like repeat of human tenascin C. The
 CC antibody, its fragment, recombinant or conjugate derivatives,
 CC immunoglobulin molecule and biotinylated derivatives are useful for a
 CC diagnostic means for detecting, or preparing a medicament for treating,
 CC diseases expressing tenascin, e.g. tumor such as gliomas, mammary, cystic brain
 CC tumors, lung carcinomas, fibrosarcomas, and squamous cell
 CC carcinomas. The diagnostic means is used in vivo imaging techniques.
 CC The medicament is in the form of a kit suitable for carrying out the
 CC three-step pre-targeting method. The antibody, in combination with a
 CC second tenascin-specific antibody are useful in sandwich assay for
 CC detecting the level of circulating tenascin. The present sequence
 CC represents the ST2146 Mab heavy chain variable region sequence
 XX
 XX Sequence 120 AA;

Query Match 84.6%; Score 548.5; DB 7; Length 120;

Best Local Similarity 86.7%; Pred. No. 6e-39;
Matches 104; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKRGASVKVSCASGATFTNNMYWKQSHGKSLWIGITDIPYGGPGY 60
DB 1 KVKLOQSGPELVKRGASVKVSCASGATFTNNMYWKQSHGKSLWIGITDIPYGGPGY 60
QY 61 SOKFKGKATLTVDKSSSTAYMHLNLSITSEDSAVYYCARRGNFPYV-PDYWGQGTTLTVSS 119
DB 61 NQFKGKATLTVDKSSSTAYMHLNLSITSEDSAVYYCARRGNFPYV-PDYWGQGTTLTVSS 120

RESULT 4
ADCC24943
ID ADCC24943 standard, protein: 140 AA.

AC ADCC24943;
XX
DT 18-DEC-2003 (first entry)

XX Mouse 19/2 antibody heavy chain variable region SEQ ID NO:28.

XX fusion protein; chimerised antibody; tumour necrosis factor; TNF;
XX antibody; chimeric fusion protein; antiinflammatory; antineumatic;
XX antiarthritic; antipsoriatic; antiasthmatic; neuoprotective; virucide;
XX rheumatoid arthritis; immunosuppressive; nephrotropic; antiarteriosclerotic;
XX inflammatory bowel disease; multiple sclerosis; psoriasis; asthma;
XX bacterial pneumonia; septic shock; nephritis; arteriosclerosis; mouse;
XX 19/2 antibody.

XX Synthetic.
XX Mus sp.

PN WO2003068924-A2.

XX 21-AUG-2003.

XX 12-FEB-2003; 2003WO-US004243.

XX 13-FEB-2002; 2002US-0355838P.

XX (LUDW-) LUDWIG INST CANCER RES.

PI Renner C, Scott A;

XX WPI; 2003-679629/64.

DR N-PSDB; ADCC24938.

XX New nucleic acid, useful for producing humanized or chimeric antibodies,
PT or fusion proteins comprising the antibodies, which are G250-specific and
PT useful for treating inflammatory conditions, e.g. rheumatoid arthritis or
PT asthma.

XX Example 2; SEQ ID NO 26; 80pp; English.

XX The present invention describes an isolated nucleic acid molecule, which
XX encodes a fusion protein comprising a chimerised antibody molecule, and a
XX tumour necrosis factor (TNF) molecule or its fragment. The antibody
XX specifically binds to a target. The fragment of the TNF molecule
XX possesses the cell killing properties of a full-length TNF molecule. Also
XX described: (1) a chimeric fusion protein (I) encoded by the isolated
XX nucleic acid molecule; (2) an expression vector comprising the isolated
XX nucleic acid molecule operably linked to a promoter; and (3) a
XX recombinant cell comprising the isolated nucleic acid molecule or the
XX expression vector. (I) has antiinflammatory, antirheumatic,
XX antiarthritic, antipsoriatic, antiasthmatic, neuoprotective, virucide,
XX antibacterial, immunosuppressive, nephrotropic and antiarteriosclerotic
XX activities. The nucleic acid is useful for the expression of proteins,
XX especially antibodies, as well as fusion proteins that incorporate the
XX antibody and a protein. The expression vector is useful in manufacturing
XX a recombinant antibody (e.g. a fully human, humanized or chimeric
XX antibody) in a eukaryotic cell. The antibody is useful in therapy.

CC particularly for targeting G250 and blocking granulocyte-macrophage
CC stimulating factor (GM-CSF), which is involved in the development of
CC rheumatoid arthritis. The antibody is useful for treating inflammatory
CC conditions, e.g. psoriasis, asthma, inflammatory bowel disease, multiple
CC sclerosis, viral or bacterial pneumonia, septic shock, nephritis, or
CC arteriosclerosis. The present sequence represents mouse 19/2 antibody
CC heavy chain variable region, which is used in an example from the present
CC invention.

XX Sequence 140 AA;

Query Match 83.5%; Score 541; DB 7; Length 140;
Best Local Similarity 82.4%; Pred. No. 3.1e-38;
Matches 98; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIQLOQSGPELVKRGASVKVSCASGATFTNNMYWKQSHGKSLWIGITDIPYGGPGY 60
DB 18 EIQLOQSGPELVKRGASVKVSCASGATFTNNMYWKQSHGKSLWIGITDIPYGGPGY 77
QY 61 SOKFKGKATLTVDKSSSTAYMHLNLSITSEDSAVYYCARRGNFPYV-PDYWGQGTTLTVSS 119
DB 78 NQFKGKATLTVDKSSSTAYMHLNLSITSEDSAVYYCARRGNFPYV-PDYWGQGTTLTVSS 136

RESULT 5
ID ADK51711 standard, protein: 140 AA.

XX ADK51711;

XX 06-MAY-2004 (first entry)

XX Murine 19/2 heavy chain variable region protein.

XX granulocyte macrophage colony stimulating factor; GM-CSF; antibody;
XX antiinflammatory; antiarthritic; antineumatic; rheumatoid arthritis;
XX inflammatory disease; murine; 19/2 heavy chain variable region; mouse.

XX Mus sp.

PN WO2003068920-A2.

XX 21-AUG-2003.

XX 12-FEB-2003; 2003WO-US004185.

XX 13-FEB-2002; 2002US-0355838P.

XX (LUDW-) LUDWIG INST CANCER RES.

PA Renner C, Scott A, Burgess A;

XX WPI; 2003-679625/64.

DR N-PSDB; ADK51710.

XX Nucleic acids encoding chimeric granulocyte macrophage colony stimulating
PT factor (GM-CSF) specific antibodies comprising a light and a heavy chain,
PT useful for blocking effects of GM-CSF on cells, e.g. in preventing
PT rheumatoid arthritis.

XX Example 2; SEQ ID NO 28; 81pp; English.

XX The invention relates to an isolated nucleic acid encoding a chimerised
XX granulocyte macrophage colony stimulating factor (GM-CSF) specific
XX antibody light chain or heavy chain. The invention further relates to: a
XX chimerised granulocyte macrophage colony stimulating factor (GM-CSF)
XX specific antibody light chain encoded by nucleotides 1357-1757 of a
XX defined sequence of 6159 bp concatenated to the amino acid sequence
XX encoded by nucleotides 1886-2203 of the 6159bp sequence; or a chimerised
XX GM-CSF specific antibody heavy chain encoded by nucleotides 1357-1764 of
XX a defined 6629 bp sequence concatenated to the amino acid sequence
XX encoded by nucleotides 1839-2825 of the 6629bp sequence. The GM-CSF
XX antibodies have antiinflammatory, antiarthritic, and antineumatic

CC activities. The GM-CSF nucleic acid is useful for blocking GM-CSF and its
 CC effects on cells, such as in preventing the development of Rheumatoid
 CC arthritis and other inflammatory diseases and conditions. This sequence
 CC represents the murine 19/2 heavy chain variable region protein of the
 CC invention.

XX Sequence 140 AA;

Query Match 83.5%; Score 541; DB 7; Length 140;
 Best Local Similarity 82.4%; Pred. No. 3,1e-38;
 Matches 98; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIQLQOSGPELVKPGASVYVSCKASGYAFTNNTWVKQSHGKSLIEWIGYIDPYGDPGY 60
 Db 18 EVQLQOSGPELVKPGASVYVSCKASGYFTFDNINHWQSHGKSLDWDIAPYSGGTGY 77
 QY 61 SOKFKGKATLTVDKSSSTAYMHLNLSIEDSAVYVCARRGNPFYFDYWGQTTLVSS 119
 Db 78 NQEFKRAATLTVDKSSSTAYMHLNLSIEDSAVYVCARRDRPFYFDYWGQTTLVSS 136

RESULT 6

AAW95481
 ID AAW95481 standard; protein; 116 AA.

XX AAW95481;

DT 29-MAR-1999 (first entry)

DE Mouse derived R13 phage antibody heavy chain pattern A genetic sequence.

KW Catalytic; antibody; phage display; immunising; phage expression vector;
 KW prodnrg; scfv.

OS Mus sp.

XX US855885-A.

PN 05-JAN-1999.

PF 14-JUL-1994; 94US-00273146.

PR 22-JAN-1993; 93US-00007684.

XX (MCCA/) MCCAFFERTY J.

PA (CHIS/) CHISWELL D.

PA (DARS/) DARSLEY M J.

PA (TITM/) TITMAS R C.

PA (MART/) MARTIN M T.

PA (SWIT/) SMITH R.

PA (FITZ/) FITZGERALD K.

PA (WILL/) WILLIAMS R O.

PI Fitzgerald K, Darley MJ, Williams RO, Smith R, Martin MT;

PT Kenten JH, Chiswell D, McCafferty J, Titmas RC;

XX N-PSDB; AAX00880.

DR WPI; 1999-105036/09.

XX Production of catalytic antibodies displayed on bacteriophages -

PT comprises generating a gene library of antibody-derived domains inserting

XX coding into a phage expression vector and isolating the catalytic

XX antibodies.

XX Example 4; Fig 12A-J; 117pp; English.

CC antigen, optionally immunising an animal with the antigen; generating a

CC library of VH and VL domains from the immunised animal; cloning the VH

CC and VL domains into a phage expression vector to generate phage display

CC antibodies; selecting phage display antibodies which bind specifically to

CC the antigen; screening the selected phage display antibodies for

CC catalytic activity to substrate; and isolating the catalytic antibodies,

CC where the phage expression vector incorporates a histidine peptide in

CC tandem with a myc peptide. The processes are used to produce catalytic

CC antibodies, which can be used for in vivo activation of a prodnrg. The

CC present sequence represents a genetic sequence of heavy chain pattern A

XX from mouse derived R13 phage antibodies

QY 1 EIQLQOSGPELVKPGASVYVSCKASGYAFTNNTWVKQSHGKSLIEWIGYIDPYGDPGY 60

Db 1 QVQLQOSGPELVKPGASVYVSCKASGYAFTNNTWVKQSHGKSLIEWIGYIDPYGGSSTY 60

QY 61 SOKFKGKATLTVDKSSSTAYMHLNLSIEDSAVYVCARRGNPFYFDYWGQTTLVSS 119

Db 61 NQEFKRAATLTVDKSSSTAYMHLNLSIEDSAVYCA--GNP-RFAFWGQTTLVSS 116

RESULT 7

AAW84093
 ID AAW84093 standard; protein; 117 AA.

XX AAW84093;

DT 15-MAR-1999 (first entry)

DE Murine vitronectin alpha-v beta-3 receptor MAb VH region.

KW Humanised antibody; monoclonal antibody; Mab; antibody engineering;

KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer;

KW metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis;

KW diabetic retinopathy; inflammation; macular degeneration; osteoporosis;

KW Paget's disease; hyperparathyroidism; hypercalcaemia; therapy;

KW immunotherapy.

OS Mus sp.

XX WO9840488-A1.

PN 17-SEP-1998.

PF 12-MAR-1998; 98WO-US004987.

PR 12-MAR-1997; 97US-0039609P.

PA (SMIK) SMITHLINE BECHAM CORP.

PI Jonak ZL, Johanson KO, Taylor AH;

XX WPI; 1999-034590/03.

XX New anti alpha v beta 3 vitronectin receptor antibodies - used for

XX immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory

XX disorders, atherosclerosis, restenosis, cancers or osteoporosis.

XX Example 13; Page 56; 97pp; English.

XX This is the amino acid sequence of the heavy chain variable region (VH)
 CC of the anti-human alpha-v beta-3 vitronectin receptor murine monoclonal
 CC antibody D12, as deduced from isolated cDNA (see AA711757). D12 VH and VL
 CC (see AA84094) show sequence similarity to Kabat VH subgroup I (see
 CC AA84095) and Kabat VK subgroup III (see AA84096), respectively.
 CC Humanised VH (see AA84097) and VL (see AA84098) were constructed by
 CC combining the framework regions of the human V region consensus sequences
 CC with complementarity determining regions of D12 (keeping some preferred
 CC murine framework residues). The humanised antibodies are specifically
 CC reactive with the human alpha-v beta-3 protein receptor and capable of
 CC neutralising the receptor. They can be used for passive immunotherapy of
 CC a disorder mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
 CC disorders or angiogenic-related disorders, such as angiogenesis
 CC associated with diabetic retinopathy, atherosclerosis and restenosis,
 CC chronic inflammatory disorders, macular degeneration, rheumatoid
 CC arthritis and cancer, e.g. solid tumour metastasis, and diseases where
 CC bone resorption is associated with pathology such as osteoporosis,
 CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
 CC osteolytic lesions produced by bone metastasis, bone loss due to
 CC immobilisation or sex hormone deficiency. They can also be used for
 CC targeted drug therapy, and for detection and diagnosis

XX Sequence 117 AA:

Query Match 81.6%; Score 529; DB 2; Length 117;
 Best Local Similarity 84.3%; Pred. No. 2.6e-37;
 Matches 102; Conservative 8; Mismatches 5; Indels 6; Gaps 2;

QY 1 EIQLQSGPELVKPGASVVKSCASGAFPTNMYWVKSHGKSLMWIGYIDPYGDPGY 60
 DB 1 EIQLQSGPELVKPGASVVKSCASGAFPTNMYWVKSHGKSLMWIGYIDPYGDPGY 60
 QY 61 SQKFKGKATLTVDKSSSTAYMHLNLSLSEDSAVYYCARR--GMPYFDYWGQSTLTVSS 118
 DB 61 NQKFKGKATLTVDKSSSTAYMHLNLSLSEDSAVFYCARQYVGSFA---YWGQSTLTVSS 116

QY 119 S 119
 DB 117 A 117

RESULT 8
 ABP96759
 ID ABP96759 standard; protein; 214 AA.

XX ABP96759;
 DT 05-JUN-2003 (first entry)

DE TSH receptor antibody 17D2 heavy chain amino acid sequence.

XX Thytotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
 KM Gene therapy; immune reaction; thyroid cancer.

OS Synthetic.

PN WO2003018632-A2.

PD 06-MAR-2003.

PF 21-AUG-2002; 2002WO-GB003831.

PR 23-AUG-2001; 2001GB-00020649.

PR 01-JUL-2002; 2002GB-00015212.

PA (RSRR-) RSR LTD.

PI Smith BR, Furmanlak J, Sanders JF;

DR WPI; 2003-290051/28.

DR N-PSDB; ACC44914.

XX New polypeptide sequence having part or all of the primary structural
 PT conformation of one or more TSH receptor epitopes, useful for treating an
 PT autoimmune disease associated with an immune reaction to a TSH receptor,
 PT e.g. thyroid cancer.

XX Claim 71; Fig 17; 196pp; English.

XX The present invention describes a polypeptide sequence comprising part or
 CC all of the primary structural conformation of one or more Thytotropin
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
 CC produced in response to a TSH receptor interact. Also described: (1) one
 CC or more receptor TSH epitopes with which the autoantibodies and/or
 CC lymphocytes interact, as with the polypeptide sequence described above;
 CC (2) a method of screening for autoantibodies or lymphocytes produced in
 CC response to a TSH receptor in a sample of body fluid obtained from a
 CC subject suspected of suffering from, susceptible to, having or recovering
 CC from autoimmune disease associated with an immune reaction to a TSH
 CC receptor; (3) a binding partner for a TSH receptor, which is capable of
 CC binding to a TSH receptor to stimulate the TSH receptor, where the
 CC binding partner does not comprise TSH or naturally produced antibodies to
 CC the TSH receptor; and (4) a combination comprising the binding partner
 CC and one or more further agents capable of stimulating thyroid tissue,
 CC and/or tissue containing a TSH receptor, for simultaneous, separate or
 CC sequential use in stimulating thyroid tissue, and/or tissue containing a
 CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
 CC gene therapy. The polypeptide, compositions and methods from the present
 CC invention can be used for treating an autoimmune disease associated with
 CC an immune reaction to a TSH receptor. The specific binding partner is
 CC useful for the manufacture of a medicament for stimulating thyroid tissue
 CC or tissue containing a TSH receptor, and for treating thyroid cancer.
 CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
 CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
 CC and VL domains given in ABP96751 to ABP96778, which are used in the
 CC exemplification of the present invention

XX Sequence 214 AA:

Query Match 81.1%; Score 525.5; DB 6; Length 214;
 Best Local Similarity 81.7%; Pred. No. 9.7e-37;
 Matches 98; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

QY 1 EIQLQSGPELVKPGASVVKSCASGAFPTNMYWVKSHGKSLMWIGYIDPYGDPGY 60
 DB 1 DVQIQSGPELVKPGASVVKSCASGAFPTNMYWVKSHGKSLMWIGYIDPYGATSY 60
 QY 61 SQKFKGKATLTVDKSSSTAYMHLNLSLSEDSAVYYCARRGNP--PYFDYWGQSTLTVSS 119
 DB 61 HQKFKGKATLTVDKSSSTAYMHLNLSLSEDSAVYYCARRMDPDMYDYGQSTLTVSS 120

RESULT 9

ABP96760
 ID ABP96760 standard; protein; 214 AA.

XX ABP96760;

DT 05-JUN-2003 (first entry)

DE TSH receptor antibody 17D2 heavy chain amino acid sequence.

XX Thytotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
 KM Gene therapy; immune reaction; thyroid cancer.

OS Synthetic.

PN WO2003018632-A2.

PD 06-MAR-2003.

PF 21-AUG-2002; 2002WO-GB003831.

PR 23-AUG-2001; 2001GB-00020649.
PR 01-JUL-2002; 2002GB-00015212.
PA (RSRR-) RSR LTD.
PI Smith BR, Furmaniak J, Sanders JP;
XX WPI; 2003-290051/28.
XX N-PSSDI; ACC44915.
XX
BS New polypeptide sequence having part or all of the primary structural
PT conformation of one or more TSH receptor epitopes, useful for treating an
PT autoimmune disease associated with an immune reaction to a TSH receptor,
e.g. thyroid cancer.

Claim 67, Fig 18; 196pp; English.

The present invention describes a polypeptide sequence comprising part or all of the primary structural conformation of one or more thyrotropin (TSH) receptor epitopes with which autoantibodies and/or lymphocytes produced in response to a TSH receptor interact. Also described: (1) one or more receptor TSH epitopes with which the autoantibodies and/or lymphocytes interact, as with the polypeptide sequence described above; (2) a method of screening for autoantibodies or lymphocytes produced in response to a TSH receptor in a sample of body fluid obtained from a subject suspected of suffering from, susceptible to, having or recovering from autoimmune disease associated with an immune reaction to a TSH receptor; (3) a binding partner for a TSH receptor, which is capable of binding to a TSH receptor to stimulate the TSH receptor, where the binding partner does not comprise TSH or naturally produced antibodies to the TSH receptor; and (4) a combination comprising the binding partner and one or more further agents capable of stimulating thyroid tissue, and/or tissue containing a TSH receptor, for simultaneous, separate or sequential use in stimulating thyroid tissue, and/or tissue containing a TSH receptor. A TSH receptor has cytostatic activity and can be used in gene therapy. The polypeptide, compositions and methods from the present invention can be used for creating an autoimmune disease associated with an immune reaction to a TSH receptor. The specific binding partner is useful for the manufacture of a medicament for stimulating thyroid tissue or tissue containing a TSH receptor, and for treating thyroid cancer. ACC44974 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH and VL domains given in ABP96751 to ABP96778, which are used in the exemplification of the present invention

SQ Sequence 214 AA;

Query Match	81.1%; Score 525.5; DB 6; Length 214;
Best Local Similarity	81.7%; Pred. No. 9.7e-37;
Matches	99; Conservative 11; Mismatches 10; Indels 1; Gaps 1

```

OY      1 EIQLQGSGPELVKPGASVKSCKASGVAFTNNMVMWVKQSHSKSLEWIGIDPYDPGY 60
        .::.:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      1 DVQIQOGSGELVPKGASVMSCKASGVFFTYNMHWMTQTHGSKSLIEWITDYPYSATSY 60
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      61 SQEKKKALITYDKSSRTAVNHLNSLSEDSAAVVYCARRNGF--PYRYDWYGOSTLTLYSS 119
        |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      61 HQKFGRKALTIVDKSSSTRVHMLNSLISEDSAIVYICARRWDMPDYANDWGOSTVTYVSS 120
        |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

RESULT 10

ABP96763	
ID	ABP96763 standard; protein; 214 AA.
AC	ABP96763;
DT	05-JUN-2003 (first entry)
DE	TSH receptor antibody 14D3 heavy chain amino acid sequence.
KW	Thyrotropin receptor; TSH receptor; epitope region; antibody;
XW	autoantibody; autoimmune disease; thyroid tissue; cytoelastic;
GN	wine therapy; immune reaction; thyroid cancer.

[illegible]

[illegible][illegible]

```

ID ADC27445 standard; protein; 117 AA.
XX
AC ADC27445;
XX
DT 18-DEC-2003 (first entry)
XX
DE TWEFF2#20 heavy chain variable region SEQ ID NO:14.
XX
KM antibody; TWEFF2#19; TWEFF2; binding inhibitor; prostate cancer;
KM cytototoxic; vaccine; primary prostate cancer; metastatic prostate cancer;
KM locally advanced prostate cancer; androgen independent prostate cancer.
XX
OS Synthetic.
XX
PN MO2003075855-A2.
XX
PD 18-SEP-2003.
XX
PF 07-MAR-2003; 2003WO-US007209.
XX
PR 08-MAR-2002; 2002US-0362837P.
XX PR 27-DEC-2002; 2002US-0436812P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
PI Bhaekar V, De la Calle A, Law D, Caras I, Ramakrishnan V,
PI Murray R, Afar D, Powers D;
XX
DR MPI: 2003-756783/71.
XX N-PsDB; ADC27444.
XX
PT New antibody that competitively inhibits binding of TWEFF219 to TWEFF2,
PT useful for treating prostate cancer, e.g. primary, metastatic, locally
PT advanced, or androgen independent prostate cancer.
XX
PS Example 1; SEQ ID NO 14; 51bp; English.
XX
CC The present invention describes an antibody (1) that competitively
CC inhibits binding of TWEFF2#19 to TWEFF2. Also described: (1) a
CC pharmaceutical composition comprising the antibody and a carrier; (2)
CC detecting a prostate cancer cell in a biological sample from a patient by
CC contacting the biological sample with the antibody; (3) inhibiting the
CC proliferation of a prostate cancer-associated cell by contacting the cell
CC with the antibody; and (4) treating prostate cancer with an antibody to
CC TWEFF2. (1) has cytostatic activity and can be used in vaccines. The
CC antibody, composition and method are useful for treating prostate cancer,
CC e.g. primary prostate cancer, metastatic prostate cancer, locally
CC advanced prostate cancer, androgen independent prostate cancer, prostate
CC cancer that has been treated with neoadjuvant therapy, or prostate cancer
CC that is refractory to treatment with neoadjuvant therapy. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 117 AA;
XX
Query Match 79.8%; Score 517; DB 7; Length 117;
Best Local Similarity 82.4%; Pred No. 2.8e-36;
Matches 98; Conservative 9; Mismatches 10; Indels 2; Gaps 1
OY 1 EIQLOQSGPELVKPGASVAVSCKASGYAFYNNYNNYVQSHGKSLIEWIGYIDYDPPG 60
DB 1 EIQLOQSGPELVKPGASVAVSCKASGYAFYNNYNNYVQSHGKSLIEWIGYIDPFNGTGY 60
OY 61 SOKFKGATLYVDKSSSTAYMELNLTSEDAVYVCARNGFFPYFPYWGCGTTLTVSS 119
DB 61 NQFKGATLYVDKSSSTAYMELNLTSEDAVYVCVYGS--DYFDYWGCGTTLTVSS 117
RESULT 14
ID ABP96756 standard; protein; 214 AA.
XX
AC ABP96756;
XX

```

```
DY      05-JUN-2003    (first entry)
DE      TSH receptor antibody 16S5 heavy chain amino acid sequence.
DM      .. Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW      autoantibody; autoimmune disease; thyroid tissue; cytosolic;
KM      gene therapy; immune reaction; thyroid cancer.
OS      Synthetic.
PN      MO2003018632-AZ.
PD      06-MAR-2003.
PF      21-AUG-2002; 2002WO-GB003831.
PR      23-AUG-2001; 2001GB-00020649.
PT      01-JUL-2002; 2002GB-00015212.
XX      (RSRR-) RSR LTD.
PA      Smith BR, Furmaniak J, Sanders JP;
PI      MPI: 2003-239051/28.
DR      N-PSTD; ACC44911.
PS      New polypeptide sequence having part or all of the primary structural
PT      conformation of one or more TSH receptor epitopes, useful for treating an
PT      autoimmune disease associated with an immune reaction to a TSH receptor,
PT      e.g. thyroid cancer.
PP      Claim 67, Fig 14; 196pp; English.
PX      The present invention describes a polypeptide sequence comprising part or
CC      all of the primary structural conformation of one or more thyrotropin
CC      (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC      produced in response to a TSH receptor interact. Also described: (1) one
CC      or more receptor TSH epitopes with which the autoantibodies and/or
CC      lymphocytes interact, as with the polypeptide sequence described above;
CC      (2) a method of screening for autoantibodies or lymphocytes produced in
CC      response to a TSH receptor in a sample of body fluid obtained from a
CC      subject suspected of suffering from, susceptible to, having or recovering
CC      from autoimmune disease associated with an immune reaction to a TSH
CC      receptor; (3) a binding partner for a TSH receptor, which is capable of
CC      binding to a TSH receptor to stimulate the TSH receptor, where the
CC      binding partner does not comprise TSH or naturally produced antibodies to
CC      the TSH receptor; and (4) a combination comprising the binding partner
CC      and one or more further agents capable of stimulating thyroid tissue,
CC      and/or tissue containing a TSH receptor, for simultaneous, separate or
CC      sequential use in stimulating thyroid tissue, and/or tissue containing a
CC      TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC      gene therapy. The polypeptide, compositions and methods from the present
CC      invention can be used for treating an autoimmune disease associated with
CC      an immune reaction to a TSH receptor. The specific binding partner is
CC      useful for the manufacture of a medicament for stimulating thyroid tissue
CC      or tissue containing a TSH receptor, and for treating thyroid cancer.
CC      AC044874 to AC044905 and ABP96719 to ABP96750 represent TSH receptor
CC      sequences, and AC044910 to AC044933 encode the TSH receptor antibody VH
CC      and VL domains given in ABP96751 to ABP96778, which are used in the
CC      exemplification of the present invention
SQ      Sequence 214 AA;
DQ      Query Match          79.7%; Score 516.5; DB 6; Length 214;
        Best Local Similarity   80.8%; Pred. No. 5.6e-36;
        Matches     97; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
```

Db 61 NQKFEKATLTVDKSSSTAYWQLNSLTSEDSAVYYCARRMDPDMYDYGQGTSTVSS 120

RESULT 15

ABP96755
ID ABP96755 standard; protein; 214 AA.

AC ABP96755;

DT 05-JUN-2003 (first entry)

XX TSH receptor antibody 16E5 heavy chain amino acid sequence.

XX Thyrotropin receptor; TSH receptor; epitope region; antibody;

KM autoantibody; autoimmune disease; thyroid tissue; cytostatic;

KM gene therapy; immune reaction; thyroid cancer.

XX Synthetic.

XX WO2003018632-A2.

XX 21-AUG-2002; 2002WO-GB003831.

XX 23-AUG-2001; 2001GB-00020649.

XX 01-JUL-2002; 2002GB-00015212.

XX (RSRR-) RSR LTD.

XX Smith BR, Furmaniak J, Sanders JF;

XX WPI; 2003-290051/28.

XX N-PSDB; ACC44910.

XX New polypeptide sequence having part or all of the primary structural

XX conformation of one or more TSH receptor epitopes, useful for treating an

XX autoimmune disease associated with an immune reaction to a TSH receptor,

XX e.g. thyroid cancer.

XX Claim 71; Fig 13; 196pp; English.

XX The present invention describes a polypeptide sequence comprising part or

XX all of the primary structural conformation of one or more thyrotropin

XX (TSH) receptor epitopes with which autoantibodies and/or lymphocytes

XX produced in response to a TSH receptor interact. Also described: (1) one

XX or more receptor TSH epitopes with which the autoantibodies and/or

XX lymphocytes interact, as with the polypeptide sequence described above;

XX (2) a method of screening for autoantibodies or lymphocytes produced in

XX response to a TSH receptor in a sample of body fluid obtained from a

XX subject suspected of suffering from, susceptible to, having or recovering

XX from autoimmune disease associated with an immune reaction to a TSH

XX receptor; (3) a binding partner for a TSH receptor, which is capable of

XX binding to a TSH receptor to stimulate the TSH receptor, where the

XX binding partner does not comprise TSH or naturally produced antibodies to

XX the TSH receptor; and (4) a combination comprising the binding partner

XX and one or more further agents capable of stimulating thyroid tissue,

XX and/or tissue containing a TSH receptor, for simultaneous, separate or

XX sequential use in stimulating thyroid tissue, and/or tissue containing a

XX TSH receptor. A TSH receptor has cytostatic activity and can be used in

XX gene therapy. The polypeptide, compositions and methods from the present

XX invention can be used for treating an autoimmune disease associated with

XX an immune reaction to a TSH receptor. The specific binding partner is

XX useful for the manufacture of a medicament for stimulating thyroid tissue

XX or tissue containing a TSH receptor, and for treating thyroid cancer.

XX ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor

XX sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH

XX and VL domains given in ABP96751 to ABP96778, which are used in the

XX exemplification of the present invention

XX Sequence 214 AA;

XX SQ

Best Local Similarity 80.8%; Pred. No. 5.6e-36;
Matches 97; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIQLOSGPELVKPGASVKVSCASGYAFTNNTWVKSHGKSLIEWIGYIDPYGDPGY 60

Db 1 DVQLVSGPELVKPGASVKVSCASGYSPFGYNHWVKSHGKSLIEWIGYIDPYGATSY 60

QY 61 SQKFKGKATLTVDKSSSTAYWQLNSLTSEDSAVYYCARRGNF--PYFPDYGQGTTLTVSS 119

Db 61 NQKFEKATLTVDKSSSTAYWQLNSLTSEDSAVYYCARRMDPDMYDYGQGTSTVSS 120

Search completed: December 29, 2004, 17:57:23

Job time : 84.7906 secs

Query Match 79.7%; Score 516.5; DB 6; Length 214;

THIS PAGE BLANK (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 17:46:45 ; Search time 16.323 Seconds

(without alignment)
701.451 Million cell updates/sec

Title: US-10-774-076-2

Perfect score: 648
Sequence: 1 EIQLOQSGPELVKRGASVKV.....GNPPYPFDYWGQGTTLTVSS 119

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR79:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	526.5	81.2	137	H32513	Ig heavy chain pre
2	518.5	80.0	119	F30502	Ig heavy chain V r
3	507.5	78.3	128	I37267	Ig heavy chain V r
4	505.5	78.0	128	C37267	Ig heavy chain V r
5	503.5	77.7	139	A27609	Ig heavy chain pre
6	499	77.0	121	F37266	Ig heavy chain V r
7	496	76.5	117	S03305	Ig heavy chain V r
8	493	76.1	117	MMMS4E	Ig heavy chain V r
9	493	76.1	140	T01407	Ig heavy chain (my
10	491.5	75.8	128	A37267	Ig heavy chain V r
11	490.5	75.7	150	PM0444	Ig heavy chain V r
12	485	74.8	117	MMMS7S	Ig heavy chain V r
13	483	74.5	121	H37266	Ig heavy chain V r
14	481	74.2	118	PM0200	anti-DNA autoantib
15	476.5	73.5	122	PH0887	Ig heavy chain V r
16	475.5	73.4	135	PS0057	Ig heavy chain pre
17	475	73.3	107	PH0971	Ig heavy chain V r
18	474.5	73.2	118	S38717	Ig heavy chain V r
19	473.5	72.6	112	S09957	Ig heavy chain V-D
20	470.5	72.6	117	S25176	Ig heavy chain V r
21	469	72.4	119	PH0099	Ig heavy chain V r
22	468.5	72.3	114	SH6319	Ig heavy chain V r
23	468.5	72.3	120	R45722	anti-glycoprotein
24	466	71.9	117	S01822	Ig heavy chain V-D
25	465	71.8	119	B53285	Ig heavy chain V a
26	464	71.6	151	PM0011	Ig heavy chain pre
27	464	71.6	138	PH0105	anti-digoxin trans
28	463.5	71.5	118	MMMS38	Ig heavy chain V r
29	463	71.5	166	PM0012	Ig heavy chain pre

30	460	71.0	118	2	S38565	Ig heavy chain V r
31	459.5	70.9	120	2	A49982	Ig heavy chain V r
32	459.5	70.9	122	2	E37267	Ig heavy chain V r
33	457	70.5	119	2	S20640	Ig heavy chain V r
34	456.5	70.4	120	2	B22769	Ig heavy chain V r
35	455.5	70.3	108	2	PH0972	Ig heavy chain V r
36	455.5	70.3	120	2	F45722	anti-glycoprotein
37	452	69.8	113	2	PH0974	Ig heavy chain V r
38	452	69.8	116	1	HVMSB1	Ig heavy chain pre
39	451.5	69.7	108	2	PH0975	Ig heavy chain V r
40	451.5	69.7	116	2	S53751	antibody Fab Jcl 1
41	451.5	69.7	118	2	PM0084	Ig heavy chain V r
42	450.5	69.5	139	1	MMMS18	Ig heavy chain pre
43	450.5	69.5	287	4	PC4402	pclb leader/Ig hea
44	450	69.4	109	2	PH0973	Ig heavy chain V r
45	450	69.4	117	1	HVMSB4	Ig heavy chain pre

ALIGNMENTS

RESULT 1
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C/Accession: H32513
R/Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A/Title: Immunoglobulin kappa 1 light chain variable region gene complex organization and
A/Reference number: A94689; MUID:88313394; PMID:3138286
A/Accession: H32513
A/Molecule type: DNA
A/Residues: 1-137 <KOP>
A/Cross-references: GB:M20831; MID:g196949; PIDN:AAA8848.1; PID:g196950
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 526.5; DB 2; Length 137;
Best Local Similarity 84.9%; Pred. No. 1.9e-39;
Matches 101; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 1 EIQLOQSGPELVKRGASVKSCASGAFNNMMYWKSGHSLKIVGYIDPYGPGY 60
DB 20 EIQLOQSGAEIVKRGASVKISCRASGYSFGYNNMVKQSHGLWIGINIPYGSISY 79
QY 61 SOKFKGATLTVDKSSSTAYMHLNSLTSPDSAVYYCARGNPPYFDYWGQGTTLTVSS 119
DB 80 NOKFKGATLTVDKSSSTAYMHLNSLTSPDSAVYYCARK-NYGSFPDYWGQGTTLTVSS 137

RESULT 2
F30502
Ig heavy chain V region (A52) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C/Accession: F30502
R/Ellac, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A/Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m.
A/Reference number: A30502; MUID:88315787; PMID:2457627
A/Accession: F30502
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <EIL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 518.5; DB 2; Length 119;
Best Local Similarity 82.8%; Pred. No. 8.2e-39;
Matches 101; Conservative 5; Mismatches 9; Indels 7; Gaps 2;

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	73.5%;	Score 476.5;	DB 2;	Length 122;
Best Local Similarity	74.6%;	Pred. NO 4 1e-35;		

Best Local Similarity 74.6%; Pred. No. 4.1e-35;
Matches 91; Conservative 11; Mismatches 17

Matches 91; Conservative 11; Mismatches 17; Indels 3; Gaps 1;

OY 1 EIQLQSGPELVKPGASVKSCAKSGLFTNTNMYWVQSHGSLIEWIGYIDPYGGDPCY 60
| : | | | | | : | | | | | : | | | | | : | | |
Db 1 EVQLQQSGPELVKPGASMKISCKASGYSTGYTNMNVNQSHGNLEEMGLINPKGVSTY 60

1 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWGLINPYKGVSTY 60

```
Oy      6  SOKFGKATITVDKSSSTAYHINSLTSEDSAVVYCARRGNG--PYFDYGGQTLLV    117
          :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 NQKPRDKATITVDKSSSTAYHELTLTSEDSAVVYCARGSYGDSDFWVGAGTIYTV    120
```

61 NQKFKDKATFTVDKSSSTAYMELLSITSEDSAVVYCARSGYGGSDSDWYFDVWGAGTTTV 120

QY 118 SS 119

Db 121 SS 122

Search completed: December 29, 2004, 18:06:55
Job time : 17.4897 secs

THIS PAGE BLANK (USPTO)


```

RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC055910; AAS5910.1; -
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003066; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-set; 3.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PSS0835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein.
RW KMW
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF86EB090 CRC64;

Query Match 77.3%; Score 501; DB 2; Length 470;
Best Local Similarity 78.7%; Pred. No. 1,9e-41;
Matches 96; Conservative 10; Mismatches 12; Indels 4; Gaps 2;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFTNYNMVWKSHGKSLKEMIGYIDPYGDPGX 60
DB 20 EVQLQDSGPELVKPGASVYKSCASGYFTGYMHWKSHGSLKEMIGLVNPSNDTSY 79
QY 61 SOKFKGKATLTVDKSSSTAYMHLNLSLSEDSAVYYCAR--KGNPFYEDYWGQGTTLTV 117
DB 80 NQKFKGKATLTVDKSSSTAYMHLNLSLSEDSAVYYCARYYSGSY-WYEDVWAGATTVTV 138
QY 118 SS 119
DB 139 SS 140

RESULT 3
Q920E8 PRELIMINARY; PRT; 120 AA.
AC Q920E8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pserin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horatidis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY07936; AAL09420.1; -.
DR HSPF: P01751; INCB.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 77.2%; Score 500; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 5e-42;
Matches 96; Conservative 7; Mismatches 15; Indels 2; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFTNYNMVWKSHGKSLKEMIGYIDPYGDPGX 60
DB 1 EVQLQDSGPELVKPGASVYKSCASGYFTGYMHWKSHGSLKEMIGLVNPSNDTSY 60
QY 61 SOKFKGKATLTVDKSSSTAYMHLNLSLSEDSAVYYCA--KGNPFYEDYWGQGTTLTVS 118
DB 61 NQKFKGKATLTVDKSSSTAYMHLNLSLSEDSAVYYCAVYYGNSPAMPAYWGQGTTLTVS 120

RESULT 4
Q6PUA7 PRELIMINARY; PRT; 472 AA.
AC Q6PUA7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
```

Expression driven by an MMTV-LTR enhancer.
 RC Strauberg R.;
 RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC018535; AAH18535.1; .
 DR InterPro; IPR003599; IG_1like.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-bet; 3.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG_C1; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KM Hypothetical protein.
 SQ SEQUENCE 472 AA; 52299 MW; 165169C23D55D4AB CRC64;
 Query Match 77.0%; Score 499; DB 2; Length 472;
 Best Local Similarity 78.0%; Pred. No. 3.1e-41;
 Matches 96; Conservative 10; Mismatches 13; Indels 4; Gaps 1;
 QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFTNMYWVWKQSHGKSLWIGYIDPYGDPGY 60
 Db 20 EVQLQDSGPELVKPGASVYKSCASGYTFSDYVHWKQSHGKSLWIGYIDPYGDPGY 79
 QY 61 SQFKKQATLTVDKSSSTAYMHLNLSLTSSESAVYYCAR---RGNPFYFDYWGQGTTLT 116
 Db 80 NQFKKQATLTVDKSSSTAYMHLNLSLTSSESAVYYCARGYISYSDYHDYWGQGTTLT 139
 QY 117 VSS 119
 Db 140 VSS 142
 RESULT 5
 ID AAH18535 PRELIMINARY; PRT; 472 AA.
 AC AAH18535;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary tumor;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strauberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shennan C.M.; Schuler G.D.;
 RA Altschul S.F.; Zeeberg B.; Bueltow K.H.; Schaefer C.F.; Bhat N.K.;
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
 RA Datchenko L.; Marsina K.; Farmer A.A.; Rubin G.M.; Hong L.;
 RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
 RA Brownstein M.J.; Uedlin T.B.; Tothilyuki S.; Cantinici P.; Prange C.;
 RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
 RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulik S.W.;
 RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
 RA Fehey J.; Helton E.; Kettman M.; Madan A.; Rodriguez S.; Sanchez A.;
 RA Whitling M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
 RA Blakeley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
 RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myere R.M.; Butterfield Y.S.;
 RA Krzywnicki M.I.; Skalek U.; Smalins D.E.; Scherch A.; Schein J.E.;
 RA Jones S.J.; Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]

SEQUENCE FROM N.A.
 RC STRAIN=Czech II; TISSUE=Mammary tumor;
 RA Strauberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018535; AAH18535.1; .
 DR InterPro; IPR003599; IG_1like.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-bet; 3.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG_C1; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KM Hypothetical protein.
 SQ SEQUENCE 472 AA; 52299 MW; 165169C23D55D4AB CRC64;
 Query Match 77.0%; Score 499; DB 2; Length 472;
 Best Local Similarity 78.0%; Pred. No. 3.1e-41;
 Matches 96; Conservative 10; Mismatches 13; Indels 4; Gaps 1;
 QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFTNMYWVWKQSHGKSLWIGYIDPYGDPGY 60
 Db 20 EVQLQDSGPELVKPGASVYKSCASGYTFSDYVHWKQSHGKSLWIGYIDPYGDPGY 79
 QY 61 SQFKKQATLTVDKSSSTAYMHLNLSLTSSESAVYYCAR---RGNPFYFDYWGQGTTLT 116
 Db 80 NQFKKQATLTVDKSSSTAYMHLNLSLTSSESAVYYCARGYISYSDYHDYWGQGTTLT 139
 QY 117 VSS 119
 Db 140 VSS 142
 RESULT 6
 ID HV12_MOUSE STANDARD; PRT; 117 AA.
 AC P01756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V region MOPC 104B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 RX MEDLINE=83075344; PubMed=816276;
 RA Kahry M.R.; Fuhrman J.S.; Schilling J.W.; Rogers J.; Sibley C.H.;
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 heavy chain constant region domains";
 RL Biochemistry 21:5415-5424 (1982).
 CC -1- MISCELLANEOUS: The sequence of the light chain of this Igm myeloma
 protein has also been determined.
 CC -1- MISCELLANEOUS: This protein binds dextran.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSP; A02039; MEMSAR.
 DR HSP; P01751; INOB.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DE Direct protein sequencing; Glycoprotein; Immunoglobulin V region.
 KW DOMAIN 116
 FT DISULFID 22 96
 FT CARBOHYD 55 55
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8AC84BE447841 CRC64;
 Query Match 76.1%; Score 493; DB 1; Length 117;
 Best Local Similarity 79.8%; Pred. No. 2.4e-41;
 Matches 95; Conservative 9; Mismatches 13; Indels 2; Gaps 1;
 QY 1 EIQLOQSGPELVKPGASVYKSCASGYAFTNMYWVWKQSHGKSLWIGYIDPYGDPGY 60
 Db 1 EVQLQDSGPELVKPGASVYKSCASGYTFSDYVHWKQSHGKSLWIGYIDPYGDPGY 79
 QY 61 SQFKKQATLTVDKSSSTAYMHLNLSLTSSESAVYYCARGYISYSDYHDYWGQGTTLT 119
 Db 80 NQFKKQATLTVDKSSSTAYMHLNLSLTSSESAVYYCARGYISYSDYHDYWGQGTTLT 139

```

Db      61 NQKFKGKATLTVDKSSSTAYVQNLSTSEDSAVYYCAR--DYDWYFDVWAGCTVTYSS 117
RESULT 7
ID      Q8VJL1      PRELIMINARY;      PRT;      123 AA.
AC      Q8VJL1;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Anti-DNA heavy chain (Fragment).
GN      Name=J558;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C3H/HeJ-1Pr;
RX      MEDLINE=96409289; PubMed=8814271;
RA      Mloch M.K., Alexander A.L., Phippen A.M., Pisetky D.S., Gilkeson G.S.;
RT      "Differences in V kappa gene utilization and VH CDR3 sequence among
RL      anti-DNA from C3H-1Pr mice and lupus mice with nephritis.";
DR      EMBL; U59154; AAB02916.1; -.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; IGV_1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER      1
FT      NON_TER      123
SQ      SEQUENCE      123 AA; 13806 MW; CC0037A806B9911E CRC64;

Query Match      75.8%; Score 491; DB 2; Length 123;
Best Local Similarity 76.8%; Pred. No. 4.1e-41;
Matches 96; Conservative 8; Mismatches 13; Indels 8; Gaps 2;

QY      1 EIQLOQSGPELVKPGASVYKSCKASGYAFNMYNMVYWKQSHGKSLWIGYIDPYGDPGY 60
Db      1 EIQLOQSGPELVKPGASVYKSCKASGYAFNMYNMVYWKQSHGKSLWIGYIDPYGDPGY 60
QY      61 SOKKKGATLTVDKSSSTAYVQNLSTSEDSAVYYCARNGFPY-----PDYWGCGTTL 114
Db      61 SOKKKGATLTVDKSSSTAYVQNLSTSEDSAVYYCARNGFPY-----PDYWGCGTTL 114
QY      115 LTVSS 119
Db      119 VTVSA 123

```

```

RA      Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA      Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Rahay J., Helton B., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA      Krzywiński M.I., Skalek U., Smailus D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=mix FVB/N;
RX      TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA      Strausberg R.;
RT      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL      EMBL; BC018455; AAH18455.1; -.
DR      HSSP; P01810; 2P8J.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003597; IG_cl.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF07654; Cl-bcl; 2.
DR      Pfam; PF00047; IGV_1.
DR      SMART; SM00406; IGV_1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS80290; IG_MHC; UNKNOWN_2.
KW      Hypothetical protein.
SQ      SEQUENCE      481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match      75.5%; Score 489.5; DB 2; Length 481;
Best Local Similarity 76.5%; Pred. No. 2.8e-40;
Matches 91; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

QY      1 EIQLOQSGPELVKPGASVYKSCKASGYAFNMYNMVYWKQSHGKSLWIGYIDPYGDPGY 60
Db      20 EIQLOQSGPELVKPGASVYKSCKASGYAFNMYNMVYWKQSHGKSLWIGYIDPYGDPGY 79
QY      61 SOKKKGATLTVDKSSSTAYVQNLSTSEDSAVYYCARNGFPYFDYWGCGTTLTVSS 119
Db      61 SOKKKGATLTVDKSSSTAYVQNLSTSEDSAVYYCARNGFPYFDYWGCGTTLTVSS 119
QY      80 NQKFKGKATLTVDKSSSTAYVQNLSTSEDSAVYYCARNGFPYFDYWGCGTTLTVSS 137
Db      80 NQKFKGKATLTVDKSSSTAYVQNLSTSEDSAVYYCARNGFPYFDYWGCGTTLTVSS 137

```

RESULT 9

HVL3 MOUSE

ID HVL3 MOUSE

STANDARD; PRT; 117 AA.

AC P01757;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DR Ig heavy chain V region J558.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE.

RX MEDLINE=80078170; PubMed=6765983;

RT Schilling J., Clevinger B., Davie J.M., Hood L.;

RT "Amino acid sequence of homogeneous antibodies to dextran and DNA

RT rearrangements in heavy chain V-region gene segments.";

RL Nature 283:35-40(1980).

CC -1- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also

CC bind dextran differ from that shown at 1-7 positions, many of

CC which occur in the D and J segments.

CC -1- SIMILARITY: This protein binds dextran.

CC PIR; A26242; MEMSJS.

DR HSSP; P01751; 1NOB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 116
 FT DISULFID 22 96 By similarity.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447B41 CRC64;

Query Match 74.8%; Score 485; DB 1; Length 117;
 Best Local Similarity 79.8%; Pred. No. 1.5e-40;
 Matches 95; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

QY 1 EIQLOOQSGPELVKRGASVYKSCASGYAFNTNMYWYKSHGKSLWIGYIDPYGPGY 60
 DB 1 EVQLQOQSGPELVKRGASVYKSCASGYFTDYMKWYKSHGKSLWIGIDINPNNGTSTY 60
 QY 61 SOKFKGKATLTVDKSSSTAYVHLNLSITSEDSAVYYCARNGFPYYPDYGQGTTLTVSS 119
 DB 61 NQKFKGKATLTVDKSSSTAYVHLNLSITSEDSAVYYCAR--DRYVYFDVWGAGTIVTVSS 117

RESULT 10

Q90XES9 PRELIMINARY; PRT; 117 AA.

AC Q90XES9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Immunoglobulin heavy chain V-D-J region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ225174; CAB65237.1; -.
 DR PIR; F33932; F33932.
 DR HSSP; P01751; 1NOB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON_TER 1 117
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13000 MW; CDD2AF4D499734 CRC64;

Query Match 74.8%; Score 485; DB 2; Length 117;
 Best Local Similarity 79.8%; Pred. No. 1.5e-40;
 Matches 95; Conservative 8; Mismatches 14; Indels 2; Gaps 1;

QY 1 EIQLOOQSGPELVKRGASVYKSCASGYAFNTNMYWYKSHGKSLWIGYIDPYGPGY 60
 DB 1 EVQLQOQSGPELVKRGASVYKSCASGYFTDYMKWYKSHGKSLWIGIDINPNNGTSTY 60
 QY 61 SOKFKGKATLTVDKSSSTAYVHLNLSITSEDSAVYYCARNGFPYYPDYGQGTTLTVSS 119
 DB 61 NQKFKGKATLTVDKSSSTAYVHLNLSITSEDSAVYYCAR--DRYVYFDVWGAGTIVTVSS 117

RESULT 11

Q91WR1 PRELIMINARY; PRT; 488 AA.

AC Q91WR1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Igh-VJ558 protein.

GN Name=Igh-VJ558;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932;

RA Straubeberg R.J., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marisina K., Farmer A.A., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Boeak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.B.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. '99;16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Kidney;

RL Straubeberg R.J.

DR EMBL; BC013539; AAH13539.1; -.

DR HSSP; P01751; 1AGW.

DR MGI; MGI:96486; Igh-VJ558.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00654; Cl-sec; 2.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IgV; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.

SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 72.5%; Score 469.5; DB 2; Length 488;
 Best Local Similarity 73.4%; Pred. No. 2.8e-38;
 Matches 91; Conservative 11; Mismatches 17; Indels 5; Gaps 1;

QY 1 EIQLOOQSGPELVKRGASVYKSCASGYAFNTNMYWYKSHGKSLWIGYIDPYGPGY 60
 DB 20 EVQLQOQSGPELVKRGASVYKSCASGYFTDYMKWYKSHGKSLWIGIDINPNNGTSTY 79
 QY 61 SOKFKGKATLTVDKSSSTAYVHLNLSITSEDSAVYYCARNGFPYYPDYGQGTTLTVSS 115
 DB 80 NQKFKGKATLTVDKSSSTAYVHLNLSITSEDSAVYYCARNGFPYYPDYGQGTTLTVSS 139

QY 116 TVSS 119
 DB 140 TVSA 143

RESULT 12

HVS1_MOUSE STANDARD; PRT; 118 AA.

AC P06330;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JUN-1988 (Rel. 06, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

```

DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovenis J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
  lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J.3:517-523(1984).
DR PIR; A02040; MMS38.
DR HSSP; P01751; INQB.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 98 V segment.
FT DOMAIN 99 104 D segment.
FT DOMAIN 105 118 J segment.
FT DISULFID 22 96 By similarity.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BBA4C62A018 CRC64;

Query Match 71.5%; Score 463.5; DB 1; Length 118;
Best Local Similarity 77.5%; Pred. No. 2.2e-38;
Matches 93; Conservative 6; Mismatches 18; Indels 3; Gaps 2;

QY 1 EIQLOQSGPELVKPGASVVKSCKASGYAFITNNYMYWKSHGKSLIEWIGYIDPYGDPGY 60
DQ 1 EVQLQSGPELVKPGASVVKSCKASGYFTFDYNNMWKSHGKSLIEWIGIDINNNGSTY 60
DB 61 SOKFKKATLTVDKSSSTAYMHLNSLTSEDSAVYTCARR-RGNPFYFDYWGQGTTLTVSS 119
QY 61 SOKFKKATLTVDKSSSTAYMHLNSLTSEDSAVYTCARR-RGNPFYFDYWGQGTTLTVSS 119
DB 61 NQKFKKATLTVDKSSSATYMLNSLTSEDSAVYTCARGYDYP--FDVNGTGYTVVSS 118

RESULT 13
Q924R8 PRELIMINARY; PRT; 146 AA.
AC Q924R8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067781; BAB63266.1; -.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.

```

```

DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 146
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16216 MW; 92460F1EDF1B7538 CRC64;

```

```

Query Match 71.3%; Score 462; DB 2; Length 146;
Best Local Similarity 74.4%; Pred. No. 3.9e-38;
Matches 90; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

QY 1 EIQLOQSGPELVKPGASVVKSCKASGYAFITNNYMYWKSHGKSLIEWIGYIDPYGDPGY 60
DQ 1 EVQLQSGPELVKPGASVVKSCKASGYFTFDYNNMWKSHGKSLIEWIGIDINNNGSTY 60
DB 61 SOKFKKATLTVDKSSSTAYMHLNSLTSEDSAVYTCARR-RGNPFYFDYWGQGTTLTVSS 118
QY 61 SOKFKKATLTVDKSSSTAYMHLNSLTSEDSAVYTCARR-RGNPFYFDYWGQGTTLTVSS 118
DB 61 NQKFKKATLTVDKSSSTAYMHLNSLTSEDSAVYTCARR-RGNPFYFDYWGQGTTLTVSS 120

QY 119 S 119
DQ 121 S 121
DB 121 S 121

```

```

RESULT 14
Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
  Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
  the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
  of the irradiated mice by treatment with the intestinal RNA of mice of
  the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAK43732.1; -.
DR HSSP; P01751; IAGW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 70.1%; Score 454; DB 2; Length 170;

```


Best Local Similarity 68.0%; Pred. No. 2.9e-37;
Matches 83; Conservative 19; Mismatches 16; Indels 4; Gaps 2;

Search completed: December 29, 2004, 18:05:16
Job time : 83.1416 secs

QY 1 EIQLOQSGPELVKPGASVKASGAFNMYMVKSHGSLKLEWIGYIDPYGDPGY 60
Db 3 QVTLQSGPEVVRPGVSVKISCKSGYTFPDYSMHMLKMHNAOSLEWIGISTYDQNTY 62
QY 61 SQKFKGKATLVDSKSTAYMHLNLSLSEDSAVYYCAR---RGNFPYPPDYWGQGTTLTV 117
Db 63 NQKFKGKATLVDSKSTAYMHLNLSLSEDSAVYYCAR---RGNFPYPPDYWGQGTTLTV 121
QY 118 SS 119
Db 122 SS 123

RESULT 15
ID HV15_MOUSE STANDARD; PRT; 136 AA.

AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;

RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; Pubmed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blatcher P.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared by
two adjacent CH genes."
RT Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
CC or send an email to license@ebi.ac.uk).

CC EMBL; J00494; AAA8130.1; -.
DR PIR; A02042; HWM5B1.
DR HSSP; P01751; INOB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 Ig heavy chain V region BCL1.
FT DOMAIN 20 135 Ig-like.
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 69.8%; Score 452; DB 1; Length 136;
Best Local Similarity 72.5%; Pred. No. 3.6e-37;
Matches 87; Conservative 11; Mismatches 18; Indels 4; Gaps 2;

QY 1 EIQLOQSGPELVKPGASVKASGAFNMYMVKSHGSLKLEWIGYIDPYGDPGY 60
Db 20 QVTLQSGPEVVRPGVSVKISCKSGYTFPDYSMHMLKMHNAOSLEWIGISTYDQNTY 79
QY 61 SQKFKGKATLVDSKSTAYMHLNLSLSEDSAVYYCAR---RGNFPYPPDYWGQGTTLTVSS 119
Db 80 NQKFKGKATLVDSKSTAYMHLNLSLSEDSAVYYCAR---RGNFPYPPDYWGQGTTLTVSS 136

THIS PAGE BLANK (uspto)